Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: __JANE ZARA__   Examiner # : __77512__   Date: __11-1-05__

Art Unit: __1635__   Phone Number: __2-0765__   Serial Number: __09/699,667__

Location (Bldg/Room#): __2D28__ (Mailbox #): __2C18__   Results Format Preferred (circle): (PAPER) DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: __NA enzyme__

Inventors (please provide full names): __J-P Perreault et al.__

Earliest Priority Date: __4-29-99__

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID Nos:

62, 65, 66

- Limit to 200 NTS.

- No size limits

- Please include interference Search.

Thanks.

****

UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

Bib Data Sheet

SERIAL NUMBER 09/699,667	FILING DATE 10/30/2000 RULE _	CLASS 435	GROUP ART UNIT 1635	ATTORNEY DOCKET NO. 77473-12

APPLICANTS

Jean-Pierre Perreault, Fleurimont, CANADA;
Sirinart Ananvoranich, Westbury, CANADA;
Daniel Lafontaine, Saint-Alexis de Montcalm, CANADA;

** CONTINUING DATA ***************************
THIS APPLICATION IS A CON OF PCT/CA99/00391 04/29/1999

** FOREIGN APPLICATIONS ***********************
CANADA 2230203 04/29/1998

IF REQUIRED, FOREIGN FILING LICENSE
GRANTED ** 01/19/2001   ** SMALL ENTITY **

Foreign Priority claimed ☒ yes ☐ no 35 USC 119 (a-d) conditions met ☒ yes ☐ no ☐ Met after Allowance Verified and Acknowledged Examiner's Signature Initials	STATE OR COUNTRY CANADA	SHEETS DRAWING 7	TOTAL CLAIMS 19	INDEPENDENT CLAIMS 1

ADDRESS

22249

TITLE

Nucleic acid enzyme for RNA cleavage

FILING FEE RECEIVED 420	FEES: Authority has been given in Paper No. _____ to charge/credit DEPOSIT ACCOUNT No. _____ for following:	☐ All Fees
		☐ 1.16 Fees (Filing)
		☐ 1.17 Fees (Processing Ext. of time)
		☐ 1.18 Fees (Issue)
		☐ Other _____
		☐ Credit _____

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10/27   95
10/28   20

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: _JANE ZARA_   Examiner # : _77512_ Date: _10 -19-05_

Art Unit: _1635_   Phone Number: _2-0765_   Serial Number: _09/699,667_

Location (Bldg/Room#): _2028_ (Mailbox #): _2C18_   Results Format Preferred (circle): (PAPER) DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____ _NA enzyme_

Inventors (please provide full names): _Perreault, J-P et d._

Earliest Priority Date: _10 - 30 -00_

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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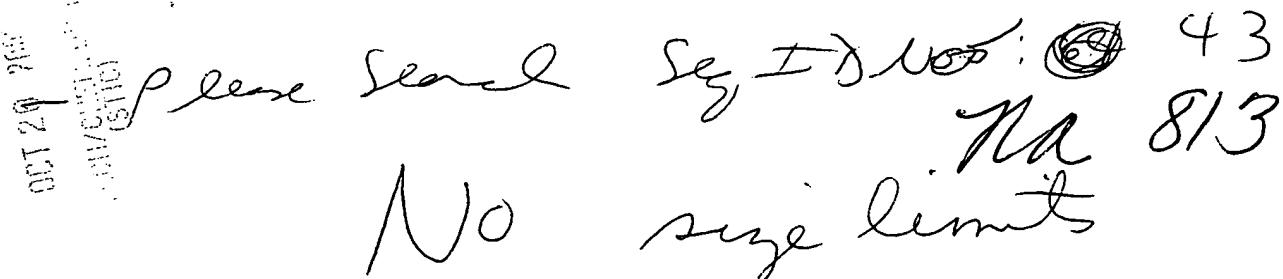
Please Search Seq ID Nos: 43
NA 813
No size limits

mej

Please Search interference database.

Thanks.

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                  GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:       October 29, 2005, 08:49:56 ; Search time 792 Seconds
                                (without alignments)
                          594.397 Million cell updates/sec

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               Gapop 10_0 , Gapext 1.0

Searched:     9784742 seqs, 412949052 residues

Total number of hits satisfying chosen parameters:     11492560

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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6	c	24.4	42.8	90	9	US-09-733-042-13	Sequence 13, Appl
7		24.4	42.8	90	10	US-09-190-246-2	Sequence 2, Appli
8	c	24.4	42.8	91	16	US-10-237-302-7	Sequence 7, Appli
9	c	24.4	42.8	99	16	US-10-237-302-8	Sequence 8, Appli
10		23	40.4	56	10	US-09-507-362-39	Sequence 39, Appl
11		23	40.4	56	18	US-10-391-441-39	Sequence 39, Appl
12		21	36.8	110	22	US-10-855-975-25	Sequence 25, Appl
13	c	20.6	36.1	130	21	US-10-425-115-163015	Sequence 163015,
14		20	35.1	45	22	US-10-430-562-5	Sequence 5, Appli
15		20	35.1	49	9	US-09-812-186-5	Sequence 5, Appli
16		20	35.1	49	10	US-09-961-077-1234	Sequence 1234, Ap
17		20	35.1	49	14	US-10-103-480-9	Sequence 9, Appli
18		20	35.1	49	16	US-10-156-433-38	Sequence 38, Appl
19		20	35.1	49	17	US-10-112-814-38	Sequence 38, Appl
20	c	19.8	34.4	60	10	US-09-908-975-6071	Sequence 6071, Ap
21	c	19.6	34.0	60	10	US-09-908-975-13039	Sequence 13039, A
22		19.4	33.3	111	22	US-10-728-131-98	Sequence 98, Appl
23		19	33.1	134	9	US-09-783-590-7012	Sequence 7012, Ap
24	c	18.4	32.3	119	10	US-09-835-976B-32	Sequence 32, Appl
25	c	18.4	32.3	135	20	US-10-437-963-2147	Sequence 2147, Ap
26		18.2	31.9	103	9	US-09-837-992-10	Sequence 10, Appl
27		18.2	31.9	103	26	US-11-128-026-10	Sequence 10, Appl
28	c	18.2	31.9	122	9	US-09-864-761-21127	Sequence 21127, A
29	c	18.2	31.9	144	21	US-10-425-115-102935	Sequence 102935,
30		18	31.6	47	19	US-10-380-438-10	Sequence 10, Appl
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32		18	31.6	60	10	US-09-908-975-20125	Sequence 20125, A
33		18	31.6	109	19	US-10-632-398-5	Sequence 5, Appli
34		18	31.6	112	18	US-10-402-841-1	Sequence 1, Appli
35	c	18	31.6	129	24	US-10-779-543-7614	Sequence 7614, Ap
36	c	18	31.6	144	20	US-10-767-701-16350	Sequence 16350, A
37		17.8	31.2	115	17	US-10-029-386-26097	Sequence 26097, A
38		17.8	31.2	123	19	US-10-425-114-4898	Sequence 4898, Ap
39	c	17.8	31.2	138	10	US-09-814-353-5007	Sequence 5007, Ap
40		17.8	31.2	138	10	US-09-814-353-11299	Sequence 11299, A
41		17.6	30.9	70	18	US-10-403-232-6	Sequence 6, Appli
42	c	17.6	30.9	75	17	US-10-259-678-163	Sequence 163, App
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44	c	17.6	30.9	142	15	US-10-010-920-10	Sequence 10, Appl
45		17.6	30.9	142	15	US-10-010-920-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
;   APPLICANT: Dubensky Jr., Thomas W
;   APPLICANT: Polo, John M
;   APPLICANT: Ibanez, Carlos E
;   APPLICANT: Chang, Stephen M.W.
;   APPLICANT: Jolly, Douglas J
;   APPLICANT: Driver, David A
;   APPLICANT: Belli, Barbara A
;   TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;   FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
;   CURRENT APPLICATION NUMBER: US/10/346,880
;   CURRENT FILING DATE: 2003-01-16
;   PRIOR APPLICATION NUMBER: 09/503,138
;   PRIOR FILING DATE: 2000-02-11
;   PRIOR APPLICATION NUMBER: 09/191,747
;   PRIOR FILING DATE: 1998-11-12
;   PRIOR APPLICATION NUMBER: 08/739,199
;   PRIOR FILING DATE: 1996-10-30
;   PRIOR APPLICATION NUMBER: 08/404,796
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: 08/376,184
;   PRIOR FILING DATE: 1995-01-18
;   PRIOR APPLICATION NUMBER: 08/348,472
;   PRIOR FILING DATE: 1994-11-30
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
		*				
1	24.4	42.8	52	18	US-10-346-880-40	Sequence 40, Appl
2	24.4	42.8	52	18	US-10-346-880-80	Sequence 80, Appl
3	24.4	42.8	52	18	US-10-150-407-40	Sequence 40, Appl
4	24.4	42.8	52	18	US-10-150-407-80	Sequence 80, Appl
5	24.4	42.8	90	9	US-09-733-042-12	Sequence 12, Appl

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;   PRIOR APPLICATION NUMBER: 08/198,450
;   PRIOR APPLICATION FILING DATE: 1994-02-18
;   PRIOR APPLICATION NUMBER: 08/122,791
;   PRIOR APPLICATION FILING DATE: 1993-09-15
;   NUMBER OF SEQ ID NOS: 128
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 40
;     LENGTH: 52
;     TYPE: DNA
;     ORGANISM: Unknown
;     FEATURE:
;     OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match             42.8%;  Score 24.4;  DB 18;  Length 52;
Best Local Similarity   59.4%;  Pred. No. 17;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy      4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
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Db      1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 2
US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
;   APPLICANT: Dubensky Jr., Thomas W
;   APPLICANT: Polo, John M
;   APPLICANT: Ibanez, Carlos E
;   APPLICANT: Chang, Stephen M.W.
;   APPLICANT: Jolly, Douglas J
;   APPLICANT: Driver, David A
;   APPLICANT: Belli, Barbara A
;   TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;   FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
;   CURRENT APPLICATION NUMBER: US/10/346,880
;   CURRENT FILING DATE: 2003-01-16
;   PRIOR APPLICATION NUMBER: 09/503,138
;   PRIOR APPLICATION FILING DATE: 2000-02-11
;   PRIOR APPLICATION NUMBER: 09/191,747
;   PRIOR APPLICATION FILING DATE: 1998-11-12
;   PRIOR APPLICATION NUMBER: 08/739,199
;   PRIOR APPLICATION FILING DATE: 1996-10-30
;   PRIOR APPLICATION NUMBER: 08/404,796
;   PRIOR APPLICATION FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: 08/376,184
;   PRIOR APPLICATION FILING DATE: 1995-01-18
;   PRIOR APPLICATION NUMBER: 08/348,472
;   PRIOR APPLICATION FILING DATE: 1994-11-30
;   PRIOR APPLICATION NUMBER: 08/198,450
;   PRIOR APPLICATION FILING DATE: 1994-02-18
;   PRIOR APPLICATION NUMBER: 08/122,791
;   PRIOR APPLICATION FILING DATE: 1993-09-15
;   NUMBER OF SEQ ID NOS: 128
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 80
;     LENGTH: 52
;     TYPE: DNA
;     ORGANISM: Unknown
;     FEATURE:
;     OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match             42.8%;  Score 24.4;  DB 18;  Length 52;
Best Local Similarity   59.4%;  Pred. No. 17;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy      4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
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Db      1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 3
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
;   APPLICANT: Dubensky Jr, Thomas W
;     Polo, John M.
;     Jolly, Douglas J.
;     Driver, David A.
;   TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;   NUMBER OF SEQUENCES: 128
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: US
;     ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/150,407
;     FILING DATE: 17-May-2002
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/350,522
;     FILING DATE: 08-Jul-1999
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McMasters, David D.
;     REGISTRATION NUMBER: 33,963
;     REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 622-4900
;     TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 52 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-150-407-40

Query Match             42.8%;  Score 24.4;  DB 18;  Length 52;
Best Local Similarity   59.4%;  Pred. No. 17;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy      4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
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Db      1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 4
US-10-150-407-80
; Sequence 80, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
;   APPLICANT: Dubensky Jr, Thomas W
;     Polo, John M.
;     Jolly, Douglas J.
;     Driver, David A.
;   TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;   NUMBER OF SEQUENCES: 128
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: US
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          ZIP: 98104-7092
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/150,407
    FILING DATE: 17-May-2002
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/350,522
    FILING DATE: 08-Jul-1999
ATTORNEY/AGENT INFORMATION:
    NAME: McMasters, David D.
    REGISTRATION NUMBER: 33,963
    REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (206) 622-4900
    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
    LENGTH: 52 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

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Best Local Similarity  59.4%;   Pred. No. 17;
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RESULT 5
US-09-733-042-12
; Sequence 12, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-FOR
US-09-733-042-12

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Best Local Similarity  59.4%;   Pred. No. 16;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

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Db   22 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 53


RESULT 6
US-09-733-042-13/c
; Sequence 13, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
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; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-REV
US-09-733-042-13

Query Match        42.8%;   Score 24.4;  DB 9;  Length 90;
Best Local Similarity  59.4%;   Pred. No. 16;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
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Db   73 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 42


RESULT 7
US-09-190-246-2
; Sequence 2, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-2

Query Match        42.8%;   Score 24.4;  DB 10;  Length 90;
Best Local Similarity  59.4%;   Pred. No. 16;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
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Db   22 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 53


RESULT 8
US-10-237-302-7
; Sequence 7, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
```

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; SEQ ID NO 7
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match       42.8%;  Score 24.4;  DB 16;  Length 91;
Best Local Similarity  59.4%;  Pred. No. 16;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  0;  Gaps  0;

Qy   4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
         :||||:||:|||:|        :|||||:|
Db  18 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 9
US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US2003011918241
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-8

Query Match       42.8%;  Score 24.4;  DB 16;  Length 99;
Best Local Similarity  59.4%;  Pred. No. 16;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  0;  Gaps  0;

Qy   4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
         :||||:||:|||:|        :|||||:||
Db  78 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 10
US-09-507-362-39
; Sequence 39, Application US/09507362
; Publication NO. US2003096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
;            Polo, John M.
;            Belli, Barbara A.
;            Schlesinger, Sondra
;            Dryga, Sergey A.
;            Frolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
;            WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;            SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-507-362-39

Query Match       40.4%;  Score 23;  DB 10;  Length 56;
Best Local Similarity  58.6%;  Pred. No. 57;
Matches  17;  Conservative  6;  Mismatches  6;  Indels  0;  Gaps  0;

Qy   4 UCCACCUCCGCGGUNNNNNUGGGCAU 32
         :||||:||:|||:|        :|||||
Db  27 TCCACCTCCTCGCGGTCCGACCTGGGCAT 55

RESULT 11
US-10-391-441-39
; Sequence 39, Application US/10391441
; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
;            Polo, John M.
;            Belli, Barbara A.
;            Schlesinger, Sondra
;            Dryga, Sergey A.
;            Frolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
;            WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;            SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,441
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
```

```
;      NAME: McMasters, David D.
;      REGISTRATION NUMBER: 33,963
;      REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 622-4900
;      TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 56 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match           40.4%;    Score 23;  DB 18;  Length 56;
Best Local Similarity 58.6%;    Pred. No. 57;
Matches   17;  Conservative   6;  Mismatches  6;  Indels  0;  Gaps  0;

Qy       4 UCCACCUCCUCGCGGUNNNNNUGGGCAU 32
           :|||||:|:||||:     :|||||
Db      27 TCCACCTCCTCGCGGTCCGACCTGGGCAT 55


RESULT 12
US-10-855-975-25
; Sequence 25, Application US/10855975
; Publication No. US20050037487A1
; GENERAL INFORMATION:
;   APPLICANT: Kawaoka, Yoshihiro
;   APPLICANT: Hamm, Stefan
;   APPLICANT: Ebihara, Hideki
;   APPLICANT: WARF - Wisconsin Alumni Research Foundation
;   TITLE OF INVENTION: Recombinant Influenza Vectors with A PolII Promoter and Ribozymes
;   TITLE OF INVENTION: Vaccines and Gene Therapy
;   FILE REFERENCE: 800.037US1
;   CURRENT APPLICATION NUMBER: US/10/855,975
;   CURRENT FILING DATE: 2004-05-27
;   PRIOR APPLICATION NUMBER: US 60/473,797
;   PRIOR FILING DATE: 2003-05-28
;   NUMBER OF SEQ ID NOS: 37
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 110
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic HDV ribozyme sequence
US-10-855-975-25

Query Match           36.8%;    Score 21;  DB 22;  Length 110;
Best Local Similarity 77.8%;    Pred. No. 3.2e+02;
Matches   21;  Conservative   0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy       4 UCCACCUCCUCGCGGUNNNNNUGGGC 30
           |||||||||||||||     |||||
Db      67 UCCACCUCCUCGCGGUCCGACCUGGGC 93


RESULT 13
US-10-425-115-163015/c
; Sequence 163015, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;   APPLICANT: La Rosa, Thomas J.
;   APPLICANT: Kovalic, David K.
;   APPLICANT: Zhou, Yihua
;   APPLICANT: Cao, Yongwei
;   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;   TITLE OF INVENTION: Plants
;   FILE REFERENCE: 38-21(53222)B
;   CURRENT APPLICATION NUMBER: US/10/425,115
;   CURRENT FILING DATE: 2003-04-28
;   NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 163015
;   LENGTH: 130
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_80243C.1
US-10-425-115-163015

Query Match           36.1%;    Score 20.6;  DB 21;  Length 130;
Best Local Similarity 49.1%;    Pred. No. 4.5e+02;
Matches   28;  Conservative   4;  Mismatches  25;  Indels  0;  Gaps  0;

Qy       1 GGGUCCACCUCCUCGCGGUNNNNNNNUGGGCAUGCGGCGCCGCUUCGGCAUGGCUAAGGGACCC 57
           ||| ||||| |||:||||:      ||||||| |  | |||  ||  |||| |||||  ||||||||
Db     112 GGGCGGCACCATGTCGGTTCTTTTTGTAGCCAAGAGCTTCCGCACAGCCGTGGGACGC 56


RESULT 14
US-10-430-562-5
; Sequence 5, Application US/10430562
; Publication No. US2005074760A1
; GENERAL INFORMATION:
;   APPLICANT: Matulic-Adamic, Jasenka
;   APPLICANT: Beigelman, Leonid
;   APPLICANT: Karpeisky, Alexander
;   APPLICANT: Jarvis, Thale
;   APPLICANT: Usman, Nassim
;   APPLICANT: DiRenzo, Anthony
;   APPLICANT: Wincott, Francine
;   TITLE OF INVENTION: ENZYMATIC NUCLEIC ACIDS CONTAINING
                        5'-AND/OR 3'-CAP STRUCTURES
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Lyon & Lyon
;     STREET: 633 West Fifth Street
;             Suite 4700
;     CITY: Los Angeles
;     STATE: California
;     COUNTRY: U.S.A.
;     ZIP: 90071-2066
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                   storage
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: IBM P.C. DOS 5.0
;     SOFTWARE: Word Perfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/430,562
;     FILING DATE: 06-May-2003
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/632,882
;     FILING DATE: April 16, 1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Warburg, Richard J.
;     REGISTRATION NUMBER: 32,327
;     REFERENCE/DOCKET NUMBER: 217/226
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (213) 489-1600
;     TELEFAX: (213) 955-0440
;     TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 45
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   FEATURE:
;     OTHER INFORMATION:      The letter "N" stands for
                              any base.
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-430-562-5
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Query Match         35.1%;   Score 20;  DB 22;  Length 45;
Best Local Similarity  96.3%;  Pred. No. 7.9e+02;
Matches   26;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        4 UCCACCUCCUCGCGGUNNNNNUGGGC 30
            ||||||||||||||||||||| ||||
Db        2 UCCACCUCCUCGCGGUNNNNNNGGGC 28
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RESULT 15
US-09-812-186-5
; Sequence 5, Application US/09812186
; Patent No. US20020052037A1
; GENERAL INFORMATION:
;   APPLICANT: BEIGELMAN, LEONID
;   TITLE OF INVENTION: NUCLEIC ACID CATALYSTS COMPRISING L-NUCLEOTIDE ANALOGS
;   FILE REFERENCE: MBHB00-922-A
;   CURRENT APPLICATION NUMBER: US/09/812,186
;   CURRENT FILING DATE: 2001-03-19
;   PRIOR APPLICATION NUMBER: 60/042,464
;   PRIOR FILING DATE: 1997-03-31
;   PRIOR APPLICATION NUMBER: 09/048,825
;   PRIOR FILING DATE: 1998-03-25
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 5
;   LENGTH: 49
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hepatitis
;   OTHER INFORMATION: Delta Virus (HDV) Ribozyme.
;   NAME/KEY: misc_feature
;   LOCATION: (18)..(24)
;   OTHER INFORMATION: all n's can represent any one of a, c, g, or u
US-09-812-186-5

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Query Match         35.1%;   Score 20;  DB 9;  Length 49;
Best Local Similarity  96.3%;  Pred. No. 7.9e+02;
Matches   26;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        4 UCCACCUCCUCGCGGUNNNNNUGGGC 30
            ||||||||||||||||||||| ||||
Db        2 UCCACCUCCUCGCGGUNNNNNNGGGC 28
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Search completed: October 29, 2005, 11:53:12
Job time : 793 secs

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         GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 29, 2005, 06:16:15 ; Search time 1294 Seconds
                                        (without alignments)
                                   72.077 Million cell updates/sec

Title:     US-09-699-667E-61
Perfect score: 57
Sequence:  1 ggguccaccuccucgcggun........uucgcauggcuaagggaccc 57

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:  1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:   1367770

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
             1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
             2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
             3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
             4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
             5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

c	Result No.	Score	% Query Match	Match Length	DB	ID	Description
	1	25.8	45.3	61	1	US-08-238-963A-18	Sequence 18, Appl
	2	24.4	42.8	52	1	US-08-741-881-40	Sequence 40, Appl
	3	24.4	42.8	52	1	US-08-741-881-80	Sequence 80, Appl
	4	24.4	42.8	52	1	US-08-739-158-40	Sequence 40, Appl
	5	24.4	42.8	52	1	US-08-739-158-80	Sequence 80, Appl
	6	24.4	42.8	52	2	US-08-739-167-40	Sequence 40, Appl
	7	24.4	42.8	52	2	US-08-739-167-80	Sequence 80, Appl
	8	24.4	42.8	52	3	US-08-404-796-40	Sequence 40, Appl
	9	24.4	42.8	52	3	US-08-404-796-80	Sequence 80, Appl
	10	24.4	42.8	52	3	US-08-931-869-40	Sequence 40, Appl
	11	24.4	42.8	52	3	US-08-931-869-80	Sequence 80, Appl
	12	24.4	42.8	52	3	US-09-350-399-40	Sequence 40, Appl
	13	24.4	42.8	52	3	US-09-350-399-80	Sequence 80, Appl
	14	24.4	42.8	52	3	US-09-236-140A-40	Sequence 40, Appl
	15	24.4	42.8	52	3	US-09-236-140A-80	Sequence 80, Appl
	16	24.4	42.8	80	1	US-08-238-963A-16	Sequence 16, Appl
	17	24.4	42.8	83	1	US-08-646-695-12	Sequence 12, Appl
	18	24.4	42.8	83	5	PCT-US96-06053-12	Sequence 12, Appl
	19	24.4	42.8	84	1	US-08-238-963A-13	Sequence 13, Appl
	20	24.4	42.8	84	1	US-08-238-963A-14	Sequence 14, Appl
	21	24.4	42.8	86	1	US-08-238-963A-6	Sequence 6, Appli
	22	24.4	42.8	90	4	US-09-554-337-2	Sequence 2, Appli
	23	24.4	42.8	90	4	US-09-733-042-12	Sequence 12, Appl
c	24	24.4	42.8	90	4	US-09-733-042-13	Sequence 13, Appl
c	25	24.4	42.8	101	6	5225337-2	Patent No. 5225337
c	26	24.4	42.8	101	6	5225337-2	Patent No. 5225337
c	27	24.4	42.8	105	2	US-08-553-619B-25	Sequence 25, Appl
c	28	24.8	42.8	105	2	US-08-553-619B-30	Sequence 30, Appl
c	29	23.6	41.4	85	1	US-08-238-963A-12	Sequence 12, Appl
	30	23.3	40.4	56	3	US-09-415-784-39	Sequence 39, Appl
	31	23.3	40.4	56	3	US-09-415-785A-39	Sequence 39, Appl
	32	23.3	40.4	56	3	US-08-944-465-39	Sequence 39, Appl
	33	23.3	40.4	56	3	US-09-415-868-39	Sequence 39, Appl
	34	23.3	40.4	56	4	US-09-415-900-39	Sequence 39, Appl
	35	23.3	40.4	56	1	US-09-507-362-39	Sequence 39, Appl
	36	23.3	40.4	71	1	US-08-238-963A-15	Sequence 15, Appl
	37	20.0	35.1	45	2	US-08-632-882-5	Sequence 5, Appli
	38	20.0	35.1	45	4	US-09-419-125-5	Sequence 5, Appli
	39	20.0	35.1	49	1	US-08-758-306-6	Sequence 6, Appli
	40	20.0	35.1	49	3	US-08-985-162-1875	Sequence 1875, Ap
	41	20.0	35.1	49	3	US-08-998-099-373	Sequence 373, App
	42	20.0	35.1	49	3	US-09-112-086B-7	Sequence 7, Appli
	43	20.0	35.1	49	3	US-08-975-238-5	Sequence 5, Appli
	44	20.0	35.1	49	3	US-09-094-381C-18	Sequence 18, Appl
	45	20.0	35.1	49	3	US-08-679-645-1234	Sequence 1234, Ap

ALIGNMENTS

```
RESULT 1
US-08-238-963A-18
; Sequence 18, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
;  APPLICANT: Been, Michael D.
;  APPLICANT: Rosenstein, Sarah P.
;  APPLICANT: Perrotta, Anne T.
;  TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
;  NUMBER OF SEQUENCES: 21
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
;   STREET: 633 West Fifth Street
;   STREET: Suite 4700
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: U.S.A.
;   ZIP: 90071-2066
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   MEDIUM TYPE: storage
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: IBM P.C. DOS 5.0
;   SOFTWARE: Word Perfect 5.1
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/238,963A
;   FILING DATE: May 5, 1994
;   CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/821,155
;   FILING DATE: January 13, 1992
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Warburg, Richard J.
;   REGISTRATION NUMBER: 32,327
;   REFERENCE/DOCKET NUMBER: 207/093
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 489-1600
;   TELEFAX: (213) 955-0440
;   TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 61 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-238-963A-18

Query Match             45.3%;  Score 25.8;  DB 1;  Length 61;
Best Local Similarity   77.4%;  Pred. No. 1.4;
Matches   41;  Conservative   0;  Mismatches   8;  Indels   4;  Gaps   1;
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Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCGGCUUCGCAGCUAAGGGACC 56
          ||||||||||||| |||||||| ||||| ||||||||||||
Db    8 UCCACCUCCUCGCGGUCCGACCUGGGGCAU----CUUCGGAUGGCUAAGGGAGC 56
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RESULT 2
US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-40

Query Match   42.8%; Score 24.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative   6; Mismatches   6; Indels   7; Gaps   0;

```
Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
          :||||||:||:|||||:      :||||||:|
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
```

RESULT 3
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-80

Query Match   42.8%; Score 24.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative   6; Mismatches   7; Indels   0; Gaps   0;

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Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
          :||||||:||:|||||:      :||||||:|
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
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RESULT 4
US-08-739-158-40
; Sequence 40, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:

```
        TELEPHONE: (206) 622-4900
        TELEFAX:  (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
  SEQUENCE CHARACTERISTICS:
     LENGTH: 52 base pairs
     TYPE: nucleic acid
     STRANDEDNESS: single
     TOPOLOGY: linear
US-08-739-158-40

Query Match     42.8%;  Score 24.4;  DB 1;  Length 52;
Best Local Similarity 59.4%;  Pred. No. 4.6;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
        :||||:|:||||:||     :  ||||:||
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 5
US-08-739-158-80
; Sequence 80, Application US/08739158
; Patent No. 5814482
  GENERAL INFORMATION:
     APPLICANT: Dubensky Jr, Thomas W
     APPLICANT: Polo, John M.
     APPLICANT: Ibanez, Carlos E.
     APPLICANT: Chang, Stephen M.W.
     APPLICANT: Jolly, Douglas J.
     APPLICANT: Driver, David A.
     TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
     NUMBER OF SEQUENCES: 128
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: SEED and BERRY LLP
     STREET: 6300 Columbia Center, 701 Fifth Avenue
     CITY: Seattle
     STATE: Washington
     COUNTRY: US
     ZIP: 98104-7092
  COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/739,158
     FILING DATE: 30-OCT-1996
     CLASSIFICATION: 514
  ATTORNEY/AGENT INFORMATION:
     NAME: McMasters, David D.
     REGISTRATION NUMBER: 33,963
     REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
  TELECOMMUNICATION INFORMATION:
     TELEPHONE: (206) 622-4900
     TELEFAX:  (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
  SEQUENCE CHARACTERISTICS:
     LENGTH: 52 base pairs
     TYPE: nucleic acid
     STRANDEDNESS: single
     TOPOLOGY: linear
US-08-739-158-80

Query Match     42.8%;  Score 24.4;  DB 1;  Length 52;
Best Local Similarity 59.4%;  Pred. No. 4.6;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
        :||||:|:||||:||     :  ||||:||
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 6
US-08-739-167-40
; Sequence 40, Application US/08739167
; Patent No. 5843723
  GENERAL INFORMATION:
     APPLICANT: Dubensky Jr, Thomas W
     APPLICANT: Polo, John M.
     APPLICANT: Ibanez, Carlos E.
     APPLICANT: Chang, Stephen M.W.
     APPLICANT: Jolly, Douglas J.
     APPLICANT: Driver, David A.
     APPLICANT: Belli, Barbara A.
     TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  AND ALPHAVIRUS
     NUMBER OF SEQUENCES: 128
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: SEED and BERRY LLP
     STREET: 6300 Columbia Center, 701 Fifth Avenue
     CITY: Seattle
     STATE: Washington
     COUNTRY: US
     ZIP: 98104-7092
  COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/739,167
     FILING DATE: 30-OCT-1996
     CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
     NAME: McMasters, David D.
     REGISTRATION NUMBER: 33,963
     REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
  TELECOMMUNICATION INFORMATION:
     TELEPHONE: (206) 622-4900
     TELEFAX:  (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
  SEQUENCE CHARACTERISTICS:
     LENGTH: 52 base pairs
     TYPE: nucleic acid
     STRANDEDNESS: single
     TOPOLOGY: linear
US-08-739-167-40

Query Match     42.8%;  Score 24.4;  DB 2;  Length 52;
Best Local Similarity 59.4%;  Pred. No. 4.6;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
        :||||:|:||||:||     :  ||||:||
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 7
US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
  GENERAL INFORMATION:
     APPLICANT: Dubensky Jr, Thomas W
     APPLICANT: Polo, John M.
     APPLICANT: Ibanez, Carlos E.
     APPLICANT: Chang, Stephen M.W.
     APPLICANT: Jolly, Douglas J.
     APPLICANT: Driver, David A.
     APPLICANT: Belli, Barbara A.
     TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  AND ALPHAVIRUS
     NUMBER OF SEQUENCES: 128
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: SEED and BERRY LLP
     STREET: 6300 Columbia Center, 701 Fifth Avenue
     CITY: Seattle
     STATE: Washington
     COUNTRY: US
     ZIP: 98104-7092
  COMPUTER READABLE FORM:
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           MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/739,167
        FILING DATE: 30-OCT-1996
        CLASSIFICATION: 435
     ATTORNEY/AGENT INFORMATION:
        NAME: McMasters, David D.
        REGISTRATION NUMBER: 33,963
        REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
     TELECOMMUNICATION INFORMATION:
        TELEPHONE: (206) 622-4900
        TELEFAX: (206) 682-6031
     INFORMATION FOR SEQ ID NO: 80:
     SEQUENCE CHARACTERISTICS:
        LENGTH: 52 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
US-08-739-167-80

Query Match           42.8%;    Score 24.4;   DB 2;  Length 52;
Best Local Similarity 59.4%;    Pred. No. 4.6;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  7;  Gaps  0;

Qy   4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
         :||||||:||:||||:      :|||||:||
Db   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 8
US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
;    APPLICANT: Dubensky Jr, Thomas W
;    APPLICANT: Polo, John M.
;    APPLICANT: Ibanez, Carlos E.
;    APPLICANT: Chang, Stephen M.W.
;    APPLICANT: Jolly, Douglas J.
;    APPLICANT: Driver, David A.
;    APPLICANT: Belli, Barbara A.
;    TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;    NUMBER OF SEQUENCES: 128
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: SEED and BERRY LLP
;       STREET: 6300 Columbia Center, 701 Fifth Avenue
;       CITY: Seattle
;       STATE: Washington
;       COUNTRY: US
;       ZIP: 98104-7092
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/404,796
;       FILING DATE: 15-MAR-1995
;       CLASSIFICATION: 435
;    ATTORNEY/AGENT INFORMATION:
;       NAME: McMasters, David D.
;       REGISTRATION NUMBER: 33,963
;       REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (206) 622-4900
;       TELEFAX: (206) 682-6031
;    INFORMATION FOR SEQ ID NO: 40:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 52 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-08-404-796-40

Query Match           42.8%;    Score 24.4;   DB 3;  Length 52;
Best Local Similarity 59.4%;    Pred. No. 4.6;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  7;  Gaps  0;

Qy   4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
         :||||||:||:||||:      :|||||:||
Db   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 9
US-08-404-796-80
; Sequence 80, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
;    APPLICANT: Dubensky Jr, Thomas W
;    APPLICANT: Polo, John M.
;    APPLICANT: Ibanez, Carlos E.
;    APPLICANT: Chang, Stephen M.W.
;    APPLICANT: Jolly, Douglas J.
;    APPLICANT: Driver, David A.
;    APPLICANT: Belli, Barbara A.
;    TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;    NUMBER OF SEQUENCES: 128
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: SEED and BERRY LLP
;       STREET: 6300 Columbia Center, 701 Fifth Avenue
;       CITY: Seattle
;       STATE: Washington
;       COUNTRY: US
;       ZIP: 98104-7092
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/404,796
;       FILING DATE: 15-MAR-1995
;       CLASSIFICATION: 435
;    ATTORNEY/AGENT INFORMATION:
;       NAME: McMasters, David D.
;       REGISTRATION NUMBER: 33,963
;       REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (206) 622-4900
;       TELEFAX: (206) 682-6031
;    INFORMATION FOR SEQ ID NO: 80:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 52 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-08-404-796-80

Query Match           42.8%;    Score 24.4;   DB 3;  Length 52;
Best Local Similarity 59.4%;    Pred. No. 4.6;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  7;  Gaps  0;

Qy   4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
         :||||||:||:||||:      :|||||:||
Db   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10
US-08-931-869-40
; Sequence 40, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
;    APPLICANT: Dubensky Jr, Thomas W
```

```
;  APPLICANT: Polo, John M.
;  APPLICANT: Ibanez, Carlos E.
;  APPLICANT: Chang, Stephen M.W.
;  APPLICANT: Jolly, Douglas J.
;  APPLICANT: Driver, David A.
;  APPLICANT: Belli, Barbara A.
;  TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;  NUMBER OF SEQUENCES: 128
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: SEED and BERRY LLP
;  STREET: 6300 Columbia Center, 701 Fifth Avenue
;  CITY: Seattle
;  STATE: Washington
;  COUNTRY: US
;  ZIP: 98104-7092
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/931,869
;  FILING DATE: 16-SEP-1997
;  CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/404,796
;  FILING DATE: 15-MAR-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: McMasters, David D.
;  REGISTRATION NUMBER: 33,963
;  REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (206) 622-4900
;  TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 40:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 52 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
US-08-931-869-40

Query Match             42.8%;    Score 24.4;   DB 3;   Length 52;
Best Local Similarity   59.4%;    Pred. No. 4.6;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy         4 UCCACCUCCUCGCGUNNNNNNUGGGCAUGCG 35
             :|||||:||:|||||:        :|||||:||
Db         1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 11
US-08-931-869-40
; Sequence 80, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
;  APPLICANT: Dubensky Jr, Thomas W
;  APPLICANT: Polo, John M.
;  APPLICANT: Ibanez, Carlos E.
;  APPLICANT: Chang, Stephen M.W.
;  APPLICANT: Jolly, Douglas J.
;  APPLICANT: Driver, David A.
;  APPLICANT: Belli, Barbara A.
;  TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;  NUMBER OF SEQUENCES: 128
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: SEED and BERRY LLP
;  STREET: 6300 Columbia Center, 701 Fifth Avenue
;  CITY: Seattle
;  STATE: Washington
;  COUNTRY: US
;  ZIP: 98104-7092
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/931,869
;  FILING DATE: 16-SEP-1997
;  CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/404,796
;  FILING DATE: 15-MAR-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: McMasters, David D.
;  REGISTRATION NUMBER: 33,963
;  REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (206) 622-4900
;  TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 80:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 52 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
US-08-931-869-80

Query Match             42.8%;    Score 24.4;   DB 3;   Length 52;
Best Local Similarity   59.4%;    Pred. No. 4.6;
Matches   19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy         4 UCCACCUCCUCGCGUNNNNNNUGGGCAUGCG 35
             :|||||:||:|||||:        :|||||:||
Db         1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 12
US-09-350-399-40
; Sequence 40, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
;  APPLICANT: Dubensky Jr, Thomas W
;             Polo, John M.
;             Jolly, Douglas J.
;             Driver, David A.
;  TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
;  NUMBER OF SEQUENCES: 128
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: SEED and BERRY LLP
;  STREET: 6300 Columbia Center, 701 Fifth Avenue
;  CITY: Seattle
;  STATE: Washington
;  COUNTRY: US
;  ZIP: 98104-7092
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/350,399
;  FILING DATE: 08-Jul-1999
;  CLASSIFICATION: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;  NAME: McMasters, David D.
;  REGISTRATION NUMBER: 33,963
;  REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (206) 622-4900
;  TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 40:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 52 base pairs
;  TYPE: nucleic acid
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        STRANDEDNESS: single
        TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-350-399-40

Query Match       42.8%;  Score 24.4;  DB 3;  Length 52;
Best Local Similarity  59.4%;  Pred. No. 4.6;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
        :|||||:||:|||||:      :||||:||
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
    APPLICANT: Dubensky Jr, Thomas W
        Polo, John M.
        Jolly, Douglas J.
        Driver, David A.
    TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
    NUMBER OF SEQUENCES: 128
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: SEED and BERRY LLP
      STREET: 6300 Columbia Center, 701 Fifth Avenue
      CITY: Seattle
      STATE: Washington
      COUNTRY: US
      ZIP: 98104-7092
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/350,399
      FILING DATE: 08-Jul-1999
      CLASSIFICATION: <Unknown>
    ATTORNEY/AGENT INFORMATION:
      NAME: McMasters, David D.
      REGISTRATION NUMBER: 33,963
      REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (206) 622-4900
      TELEFAX: (206) 682-6031
  INFORMATION FOR SEQ ID NO: 80:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 52 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80

Query Match       42.8%;  Score 24.4;  DB 3;  Length 52;
Best Local Similarity  59.4%;  Pred. No. 4.6;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
        :|||||:||:|||||:      :||||:||
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14
US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
    APPLICANT: Dubensky Jr, Thomas W
        Polo, John M.
        Ibanez, Carlos E.
        Chang, Stephen M.W.
        Jolly, Douglas J.
        Driver, David A.
        Belli, Barbara A.
    TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
    NUMBER OF SEQUENCES: 124
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
      STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
      CITY: NEWPORT BEACH
      STATE: CALIFORNIA
      COUNTRY: US
      ZIP: 92660
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/236,140A
      FILING DATE: 22-Jan-1999
      CLASSIFICATION: <Unknown>
    ATTORNEY/AGENT INFORMATION:
      NAME: Cullman, Louis C.
      REGISTRATION NUMBER: 39,645
      REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (949) 823.6000
      TELEFAX: (949) 823.6100
  INFORMATION FOR SEQ ID NO: 40:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 52 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-236-140A-40

Query Match       42.8%;  Score 24.4;  DB 3;  Length 52;
Best Local Similarity  59.4%;  Pred. No. 4.6;
Matches  19;  Conservative  6;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
        :|||||:||:|||||:      :||||:||
Db    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15
US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
    APPLICANT: Dubensky Jr, Thomas W
        Polo, John M.
        Ibanez, Carlos E.
        Chang, Stephen M.W.
        Jolly, Douglas J.
        Driver, David A.
        Belli, Barbara A.
    TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
    NUMBER OF SEQUENCES: 124
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
      STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
      CITY: NEWPORT BEACH
      STATE: CALIFORNIA
      COUNTRY: US
      ZIP: 92660
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/236,140A
   FILING DATE: 22-Jan-1999
   CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
   NAME: Cullman, Louis C.
   REGISTRATION NUMBER: 39,645
   REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (949) 823.6000
   TELEFAX: (949) 823.6100
INFORMATION FOR SEQ ID NO: 80:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 52 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
   SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match   42.8%;   Score 24.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy   4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
        :|||||:|:|||||:   :||||||:||
Db   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

Search completed: October 29, 2005, 10:01:36
Job time : 1294 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2005, 01:27:07 ; Search time 451 Seconds
(without alignments)
748.171 Million cell updates/sec

Title: US-09-699-667E-61
Perfect score: 57
Sequence: 1 ggguccaccuccgcggun.........uucgcauggcuaagggaccc 57

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 439206 seqs, 295987067 residues

Total number of hits satisfying chosen parameters: 4723312

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
  1: geneseqn1980s:*
  2: geneseqn1990s:*
  3: geneseqn2000s:*
  4: geneseqn2001as:*
  5: geneseqn2001bs:*
  6: geneseqn2002as:*
  7: geneseqn2002bs:*
  8: geneseqn2003as:*
  9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	51	89.5	57	3	AAZ57636	Aaz57636 Trans-act
2	51	89.5	57	3	AAZ57637	Aaz57637 Trans-act
3	41.4	72.6	57	3	AAZ57638	Aaz57638 Trans-act
4	29.4	51.6	37	3	AAZ57639	Aaz57639 Nucleotid
5	25.8	45.3	61	13	AAQ46667	Aaq46667 Substrate
6	24.4	42.8	48	13	ADR47040	Adr47040 Dengue vi
7	24.4	42.8	48	13	ADT48965	Adt48965
8	24.4	42.8	51	2	AAQ86173	Aaq86173 Primer HD
9	24.4	42.8	52	2	AAQ86204	Aaq86204 Sindbis/H
10	24.4	42.8	52	2	AAT31151	Aat31151 HDV rever
11	24.4	42.8	52	2	AAT30817	Aat30817 HDV riboz
12	24.4	42.8	52	2	AAV42394	Aav42394 Nested PC
13	24.4	42.8	52	2	AAV42426	Aav42426 Forward P
14	24.4	42.8	52	2	AAV60154	Aav60154 Nested PC
15	24.4	42.8	52	2	AAV60185	Aav60185 Reverse P
16	24.4	42.8	52	2	AAV70746	Aav70746 Reverse P
17	24.4	42.8	52	2	AAV70714	Aav70714 Nested pr
18	24.4	42.8	52	3	AAZ92930	Aaz92930 Hepatitis
19	24.4	42.8	52	3	AAZ92970	Aaz92970 Hepatitis
20	24.4	42.8	52	3	AAZ92843	Aaz92843 Hepatitis
21	24.4	42.8	52	3	AAZ92803	Aaz92803 Hepatitis
22	24.4	42.8	52	6	AAL38850	Aal38850 Alphaviru
23	24.4	42.8	52	6	AAL38810	Aal38810 Alphaviru
24	24.4	42.8	52	6	ABK46276	Abk46276 HDV antig
25	24.4	42.8	52	6	ABK46316	Abk46316 Hepatitis
26	24.4	42.8	52	12	ADI30383	Adi30383 Hepatitis
27	24.4	42.8	52	12	ADI30423	Adi30423 Hepatitis
28	24.4	42.8	52	12	ADO13982	Ado13982 Eukaryoti
29	24.4	42.8	52	12	ADO13942	Ado13942 Eukaryoti
30	24.4	42.8	57	12	ADH10551	Adh10551 Hepatitis
31	24.4	42.8	80	2	AAQ53118	Aaq53118 Substrate
32	24.4	42.8	80	2	AAQ53140	Aaq53140 Substrate
33	24.4	42.8	83	5	AAF28121	Aaf28121 HDV riboz
34	24.4	42.8	84	13	ADR47033	Adr47033 Dengue vi
35	24.4	42.8	85	2	AAQ46665	Aaq46665 Self-clea
36	24.4	42.8	86	2	AAQ46663	Aaq46663 Self-clea
37	24.4	42.8	90	2	AAX76586	Aax76586 Hepatitis
38	24.4	42.8	90	5	AAF84035	Aaf84035 EPO gene
39 c	24.4	42.8	90	5	AAF84036	Aaf84036 EPO gene
40	24.4	42.8	91	8	ABZ82120	Abz82120 Hepatitis
41	24.4	42.8	94	12	ADP96249	Adp96249 HEP rabie
42 c	24.4	42.8	99	8	ABZ82121	Abz82121 Hepatitis
43	23	40.4	56	2	AAX59264	Aax59264 Nested pr
44	23	40.4	56	2	AAX58506	Aax58506 Nested pr
45	23	40.4	56	8	ABX81463	Abx81463 Sindbis v

ALIGNMENTS

RESULT 1
AA257636
ID   AAZ57636 standard; RNA; 57 BP.
XX
AC   AAZ57636;
XX
DT   05-APR-2000 (first entry)
XX
DE   Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
XX
KW   Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW   inherited disease; deltaRzP1.1; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   misc_binding   1..6
FT   /*tag= a
FT   /note= "Forms double stranded region with bases 52-57"
FT   stem_loop   7..19
FT   /*tag= b
FT   misc_binding   20..25
FT   /*tag= c
FT   /bound_moiety= "SP1.1 substrate (AAZ57641) bases 5-11"
FT   stem_loop   30..45
FT   /*tag= d
FT   misc_binding   52..57
FT   /*tag= e
FT   /note= "Forms a double stranded region with bases 6-1"
XX
PN   WO995856-A2.
XX
PD   04-NOV-1999.
XX
PF   29-APR-1999; 99WO-CA000391.
XX
PR   29-APR-1998; 98CA-02230203.
XX
PA   (UYSH) UNIV SHERBROOKE.
XX
PI   Perreault J, Ananvoranich S, Lafontaine D;
XX
DR   WPI; 2000-096791/08.

XX
PT   New construction of nucleic acid enzyme useful for biotechnological,
PT   diagnostic and therapeutic applications.
XX
PS   Example 1; Fig 1A; 52pp; English.
XX
CC   This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
CC   cleaves substrate SP1.1 (see AAZ57641). The invention relates to a
CC   nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC   substrate binding portion with the following sequence 3'-UNNXNN-5'. The
CC   substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC   portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC   cleavage site of the substrate (cleavage site is represented by *). At
CC   least one nucleotide is present 5' to the cleavage site of the substrate
CC   sequence. The enzyme of the invention is used to cleave a substrate
CC   nucleotide sequence at a specific cleavage site by mixing the substrate
CC   with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC   for example an inherited disease. The enzymes also have other
CC   therapeutic, biotechnological and diagnostic applications
XX
SQ   Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match   89.5%; Score 51; DB 3; Length 57;
Best Local Similarity   89.5%;   Pred. No. 9e-09;
Matches   51; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 GGGUCCACCUCCUCGCGGUNNNNNNUGGGCAUGCGGCGUUCCGCCAUGGCUAAGGGACCC 57
         ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1 GGGUCCACCUCCUCGCGGUCCGACCUGGGCAUGCGGCGUUCCGCCAUGGCUAAGGGACCC 57

RESULT 2
AAZ57637
ID   AAZ57637 standard; RNA; 57 BP.
XX
AC   AAZ57637;
XX
DT   05-APR-2000 (first entry)
XX
DE   Trans-acting antigenomic delta ribozyme, deltaRzP1.2 nucleotide sequence.
XX
KW   Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW   inherited disease; deltaRzP1.2; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   misc_binding   1..6
FT   /*tag= a
FT   /note= "Forms double stranded region with bases 52-57"
FT   stem_loop   7..19
FT   /*tag= b
FT   misc_binding   20..25
FT   /*tag= c
FT   /bound_moiety= "SP1.2 substrate bases (AAZ57634) 6-11"
FT   stem_loop   30..45
FT   /*tag= d
FT   misc_binding   52..57
FT   /*tag= e
FT   /note= "Forms a double stranded region with bases 6-1"
XX
PN   WO9955856-A2.
XX
PD   04-NOV-1999.
XX
PF   29-APR-1999; 99WO-CA000391.
XX
PR   29-APR-1998; 98CA-02230203.
XX
PA   (UYSH) UNIV SHERBROOKE.
XX
PI   Perreault J, Ananvoranich S, Lafontaine D;
XX

DR   WPI; 2000-096791/08.
XX
PT   New construction of nucleic acid enzyme useful for biotechnological,
PT   diagnostic and therapeutic applications.
XX
PS   Example 1; Page; 52pp; English.
XX
CC   This is the nucleotide sequence of ribozyme deltaRzP1.2. This ribozyme
CC   cleaves substrate SP1.2 (see AAZ57634). The invention relates to a
CC   nucleic acid enzyme (e.g. deltaRzP1.2) that is constructed to have a
CC   substrate binding portion with the following sequence 3'-UNNXNN-5'. The
CC   substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC   portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC   cleavage site of the substrate (cleavage site is represented by *). At
CC   least one nucleotide is present 5' to the cleavage site of the substrate
CC   sequence. The enzyme of the invention is used to cleave a substrate
CC   nucleotide sequence at a specific cleavage site by mixing the substrate
CC   with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC   for example an inherited disease. The enzymes also have other
CC   therapeutic, biotechnological and diagnostic applications. Note: This
CC   sequence is not shown in the specification, but has been derived from the
CC   deltaRzP1.1 sequence (AAZ57636) shown in figure 1
XX
SQ   Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match   89.5%; Score 51; DB 3; Length 57;
Best Local Similarity   89.5%;   Pred. No. 9e-09;
Matches   51; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 GGGUCCACCUCCUCGCGGUNNNNNNUGGGCAUGCGGCGUUCCGCCAUGGCUAAGGGACCC 57
         ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1 GGGUCCACCUCCUCGCGGUCCGACCUGGGCAUGCGGCGUUCCGCCAUGGCUAAGGGACCC 57

RESULT 3
AAZ57638
ID   AAZ57638 standard; RNA; 57 BP.
XX
AC   AAZ57638;
XX
DT   15-SEP-2003 (revised)
DT   05-APR-2000 (first entry)
XX
DE   Trans-acting antigenomic delta ribozyme nucleotide sequence.
XX
KW   Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW   inherited disease; ss.
XX
OS   Hepatitis D virus.
XX
FH   Key   Location/Qualifiers
FT   misc_binding   1..6
FT   /*tag= a
FT   /note= "Forms double stranded region with bases 52-57"
FT   stem_loop   7..19
FT   /*tag= b
FT   misc_binding   20..25
FT   /*tag= c
FT   /bound_moiety= "SP1.1 substrate bases (AAZ57641) 5-11"
FT   stem_loop   30..45
FT   /*tag= d
FT   misc_binding   52..57
FT   /*tag= e
FT   /note= "Forms a double stranded region with bases 6-1"
XX
PN   WO9955856-A2.
XX
PD   04-NOV-1999.
XX
PF   29-APR-1999; 99WO-CA000391.
XX
PR   29-APR-1998; 98CA-02230203.
XX

```
PA   (UYSH ) UNIV SHERBROOKE.
XX
PI   Perreault J, Ananvoranich S, Lafontaine D;
XX
DR   WPI; 2000-096791/08.
XX
PT   New construction of nucleic acid enzyme useful for biotechnological,
PT   diagnostic and therapeutic application.
XX
PS   Example 1; Fig 2; 52pp; English.
XX
CC   This is the nucleotide sequence of a trans-acting antigenomic delta
CC   ribozyme of the invention. This ribozyme cleaves substrate SP1.1 (see
CC   AAZ57641).The invention relates to a nucleic acid enzyme (e.g.
CC   deltaRzp1.1) that is constructed to have a substrate binding portion with
CC   the following sequence 3'-UNNXNN-5'. The substrate of the enzyme has the
CC   sequence 5'-H'*GNNHNN-3'. The binding portion of the enzyme (ribozyme)
CC   base pairs to 6 nucleotides 3' to the cleavage site of the substrate
CC   (cleavage site is represented by *). At least one nucleotide is present
CC   5' to the cleavage site of the substrate sequence. The enzyme of the
CC   invention is used to cleave a substrate nucleotide sequence at a specific
CC   cleavage site by mixing the substrate with the enzyme. The enzyme is used
CC   to cleave viral RNA or other therapeutic, biotechnological and diagnostic
CC   enzymes also have other therapeutic, biotechnological and diagnostic
CC   applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ   Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match    72.6%;    Score 41.4;   DB 3;   Length 57;
Best Local Similarity   78.9%;   Pred. No. 2.6e-05;
Matches   45;  Conservative    0;  Mismatches   12;  Indels   0;  Gaps   0;

Qy     1 GGGUCCACCUCCUCGCGGUNNNNNNUGGGCAUGGGCCUUCGCAUGGCUAAGGGACCC 57
         ||||||||||||||||||      ||||||  ||||||||||||||||||||||||||
Db     1 GGGUCCACCUCCUCGCGGUCCGACCUGGGCAUGGGCCUUCGCAUGGCUAAGGGACCC 57

RESULT 4
AAZ57639
ID   AAZ57639 standard; RNA; 37 BP.
XX
AC   AAZ57639;
XX
DT   05-APR-2000  (first entry)
XX
DE   Nucleotide sequence of bimolecular ribozyme RzA fragment.
XX
KW   Bimolecular ribozyme; viral RNA cleavage; RzA fragment;
KW   inherited disease; ss.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   misc_binding   1..6
FT                  /*tag= a
FT                  /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT                  /note= "Forms double-stranded region with bases 20-16 of
FT                  sequence AAZ57640"
FT   stem_loop      7..19
FT                  /*tag= b
FT   misc_binding   20..25
FT                  /*tag= c
FT                  /bound_moiety= "Ribozyme substrate P1.1"
FT                  /note= "Forms double-stranded region with bases 11-6 of
FT                  sequence AAZ57641"
FT   misc_binding   30..37
FT                  /*tag= d
FT                  /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT                  /note= "Forms double-stranded region with bases 8-1 of
FT                  sequence AAZ57640"
XX
PN   WO9955856-A2.
XX


PD   04-NOV-1999.
XX
PF   29-APR-1999;    99WO-CA000391.
XX
PR   29-APR-1998;    98CA-02230203.
XX
PA   (UYSH ) UNIV SHERBROOKE.
XX
PI   Perreault J, Ananvoranich S, Lafontaine D;
XX
DR   WPI; 2000-096791/08.
XX
PT   New construction of nucleic acid enzyme useful for biotechnological,
PT   diagnostic and therapeutic applications.
XX
PS   Example 5; Fig 4; 52pp; English.
XX
CC   This is the nucleotide sequence bimolecular ribozyme RzA fragment. This
CC   ribozyme cleaves substrate SP1.1 (see AAZ57641). The invention relates to
CC   a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC   substrate binding portion with the following sequence 3'-UNNXNN-5'. The
CC   substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC   portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC   cleavage site of the substrate (cleavage site is represented by *). At
CC   least one nucleotide is present 5' to the cleavage site of the substrate
CC   sequence. The enzyme of the invention is used to cleave a substrate
CC   nucleotide sequence at a specific cleavage site by mixing the substrate
CC   with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC   for example an inherited disease. The enzymes also have other
CC   therapeutic, biotechnological and diagnostic applications
XX
SQ   Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;

Query Match    51.6%;    Score 29.4;   DB 3;   Length 37;
Best Local Similarity   81.1%;   Pred. No. 0.5;
Matches   30;  Conservative    0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     1 GGGUCCACCUCCUCGCGGUNNNNNNUGGGCAUGGGCCGGC 37
         |||||||||||||||||||      |||||||||||||
Db     1 GGGUCCACCUCCUCGGUCCGACCUGGGCCAUGCGCC 37

RESULT 5
AAQ46667
ID   AAQ46667 standard; RNA; 61 BP.
XX
AC   AAQ46667;
XX
DT   25-MAR-2003  (revised)
DT   13-JAN-1994  (first entry)
XX
DE   Substrate-cleaving sequence ADC3.
XX
KW   Substrate; self-cleaving sequence; HDV; hepatitis delta virus; enzyme;
KW   duplex; ss.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   stem_loop      7..55
FT                  /*tag= a
FT   misc_structure 7..10
FT                  /*tag= b
FT                  /label= stem_II
FT                  /note= "forms duplex with region 52. .55"
FT   stem_loop      11. .23
FT                  /*tag= d
FT   misc_structure 11. .13
FT                  /*tag= e
FT                  /label= stem_III
FT                  /note= "forms duplex with region 21. .23"
FT   misc_feature   21. .23
FT                  /*tag= f
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FT   /label= stem III
FT   /note= "forms duplex with region 11. .13"
FT   misc_structure 24. .30
FT   /*tag= g
FT   /note= "RNA substrate binding region"
FT   misc_structure 33. .37
FT   /*tag= i
FT   /label= stem IV
FT   /note= "forms duplex with region 42. .45"
FT   stem_loop 34. .45
FT   /*tag= h
FT   misc_feature 42. .45
FT   /*tag= j
FT   /label= stem IV
FT   misc_feature 52. .55
FT   /*tag= c
FT   /label= stem II
FT   /note= "forms duplex with region 7. .10"
XX
PN   WO9314218-A1.
XX
PD   22-JUL-1993.
XX
PF   12-JAN-1993; 93WO-US000292.
XX
PR   13-JAN-1992; 92US-00821155.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Been MD, Rosenstein SP, Perrota AT;
XX
DR   WPI; 1993-243233/30.
XX
PT   Nucleic acid molecule having RNA substrate-cleaving enzymatic activity -
PT   useful for cleaving specific target molecules in-vitro.
XX
PS   Disclosure; Fig 8; 55pp; English.
XX
CC   The self-cleaving sequences from genomic and antigenomic HDV can be used
CC   to develop enzymatic RNA mols. with similar properties. ADC3 is a smaller
CC   version of ADC1 (AAQ53138), wherein stem IV is shortened. Such a smaller
CC   enzymatic RNA has simplified synthesis and the potential for higher
CC   specific activity due to a higher probability that a small RNA will fold
CC   into an enzymatically active structure. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 61 BP; 10 A; 20 C; 19 G; 0 T; 12 U; 0 Other;

Query Match   45.3%;   Score 25.8;   DB 2;   Length 61;
Best Local Similarity   77.4%;   Pred. No. 11;
Matches   41;   Conservative   0;   Mismatches   8;   Indels   4;   Gaps   1;

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Qy  4 UCCACCUCCUCGCGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACC 56
        ||||||||||||||       ||||| ||||||||||||||||
Db  8 UCCACCUCCUCGCGUCCGACCUGGGCAU----CUCGGAUGGCUAAGGGAGC 56
```

RESULT 6
ADR47040
ID   ADR47040 standard; DNA; 48 BP.
XX
AC   ADR47040;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Dengue virus vaccine oligonucleotide #15.
XX
KW   ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
KW   preM protein; C protein; NS1 protein signal; vaccine; cervical cancer;
KW   viral disease; antigen; dendritic cell; immune response;
KW   human papillomavirus

OS   Unidentified.
XX
PN   WO2004072274-A1.
XX
PD   26-AUG-2004.
XX
PF   30-JAN-2004; 2004WO-CN000088.
XX
PR   30-JAN-2003; 2003CN-00115272.
PR   30-JAN-2003; 2003CN-00115273.
XX
PA   (SHAN-) SHANGHAI TENGEN BIOMEDICAL CO LTD.
PA   (TENG-) TENGEN BIOMEDICAL CO.
PA   (BEIJ-) BEIJING ORIENTAL TENGEN TECHNOLOGY DEV C.
XX
PI   Pang X;
XX
DR   WPI; 2004-625870/60.
XX
PT   Virus-like particle vaccines containing dengue virus recombinant replicon
PT   as core for carrier, applicable in preventives or/and remedies for tumors
PT   like cervical cancer and viral diseases.
XX
PS   Example 4; SEQ ID NO 37; 38pp; Chinese.
XX
CC   A dengue virus recombinant replicon has a deletion of the complete coding
CC   sequence for preM protein of dengue virus and also includes elements of
CC   e.g. the non-coding region in the whole of the 5'-end, the coding region
CC   of the front 20 amino acids in the C protein, and the coding region of
CC   NS1 protein signal; coding regions of all non-structural proteins. The
CC   obtained vaccines are useful in producing preventives or/and remedies for
CC   cancer like cervical cancer and viral diseases. Such vaccines can
CC   efficiently express antigen in infected cells, which is because dengue
CC   virus can infect dendritic cells, and can effectively present antigen to
CC   provide immunity effect. Different types of dengue virus can be used to
CC   repeatedly produce efficient immune response thereby strengthening the
CC   body's immune system against the pathogen that contains such antigen.
CC   Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC   expressing system using of the full-length dengue virus cDNA clone
CC   (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC   hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC   lines. This sequence corresponds to an oligonucleotide used in the
CC   recombinant replicon of the invention.
XX
SQ   Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;

Query Match   42.8%;   Score 24.4;   DB 13;   Length 48;
Best Local Similarity   59.4%;   Pred. No. 33;
Matches   19;   Conservative   6;   Mismatches   7;   Indels   0;   Gaps   0;

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Qy  4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCGG 35
        ||||||||||||||:||||||||||  :||||||||
Db 17 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 48
```

RESULT 7
ADT48965
ID   ADT48965 standard; DNA; 48 BP.
XX
AC   ADT48965;
XX
DT   16-DEC-2004 (first entry)
XX
DE   PCR primer 5' HDVr, seq id 29.
XX
KW   virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
KW   PCR; primer; ss.
XX
OS   Viruses.
XX
PN   WO2004082712-A1.
XX
PD   30-SEP-2004.

Left column:

XX	
PF	19-MAR-2004; 2004WO-CN000232.
XX	
PR	20-MAR-2003; 2003CN-00115912.
XX	
PA	(SHAN-) SHANGHAI TENGEN BIOMEDICAL CO LTD.
PA	(TENG-) TENGEN BIOMEDICAL CO.
PA	(BEIJ-) BEIJING ORIENTAL TENGEN TECHNOLOGY DEV C.
XX	
PI	Pang X;
XX	
DR	WPI; 2004-699719/68.
XX	

PT Bivalent vaccines for preventing and treating Japanese (B) encephalitis
PT and hepatitis B produced by recombinant technique using encephalitis B
PT virus as vector to express antigen gene of hepatitis B.

XX
PS Example 8; SEQ ID NO 29; 33pp; Chinese.
XX

CC The invention relates to a recombinant Japanese encephalitis B virus
CC constructed from encephalitis B virus and a recombinant genome, where the
CC genome is inserted with an exogenous nucleotide sequence for
CC recombination and capable of retaining its self-replication function. The
CC virus is useful in producing the bivalent vaccines for preventing and
CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are
CC producible at low cost and have high immunoefficiency, in which the
CC recombinant virus can efficiently express the antigen of hepatitis B
CC virus with the safety and immunogenicity of attenuated encephalitis B
CC virus vaccines. The current sequence represents a PCR primer used in an
CC example from the invention.
XX

SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;

```
      Query Match     42.8%;  Score 24.4;  DB 13;  Length 48;
      Best Local Similarity   59.4%;  Pred. No. 33;
      Matches  19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
         :|||||:||:||||||:  :||||||: ||
Db    17 TCCACCTCCTCGGGTCCGACCTGGGCATCCG 48
```

Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;

RESULT 8
AAQ86173
ID AAQ86173 standard; DNA; 51 BP.
XX
AC AAQ86173;
XX
DT 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX
DE Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
XX
KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
KW transcription initiation; non-structural protein; subgenomic fragment;
KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
KW primer; polymerase chain reaction; cystic fibrosis; ss.
XX
OS Synthetic.
XX
PN WO9507994-A2.
XX
PD 23-MAR-1995.
XX
PF 15-SEP-1994; 94WO-US010469.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
XX
PA (VIAG-) VIAGENE INC.
XX
PI Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
XX

Right column:

DR	WPI; 1995-131362/17.
XX	

PT New alpha virus vectors for gene therapy - of viral infection, cancer,
PT auto:immune disease, etc., and as vaccines.
XX
PS Example 2; Page 68; 260pp; English.
XX

CC The sequences given in AAQ86167-81 are primers which were used in the
CC generation of plasmid DNA which initiate Sindbis infection. The
CC amplified DNA sequences were used in the construction of a eukaryotic
CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
CC comprise a 5' sequence capable of initiating transcription of an
CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
CC proteins, a viral junction region which has been inactivated such that
CC viral transcription of the subgenomic fragment is prevented, and an
CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral
CC junction region prevents transcription of the subgenomic fragment making
CC vectors such as this suitable for a wide variety of applications, eg.
CC gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX

SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;

```
      Query Match     42.8%;  Score 24.4;  DB 2;  Length 51;
      Best Local Similarity   59.4%;  Pred. No. 33;
      Matches  19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     4 UCCACCUCCUCGCGGUNNNNNNUGGGCAUGCG 35
         :|||||:||:||||||:   :||||||:  ||
Db     1 TCCACCTCCTCGGGTCCGACCTGGGCATCCG 32
```

RESULT 9
AAQ86204
ID AAQ86204 standard; DNA; 52 BP.
XX
AC AAQ86204;
XX
DT 25-MAR-2003 (revised)
DT 23-NOV-1995 (first entry)
XX
DE Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.
XX
KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
KW transcription initiation; non-structural protein; subgenomic fragment;
KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
KW primer; polymerase chain reaction; cystic fibrosis; ss.
XX
OS Synthetic.
XX
PN WO9507994-A2.
XX
PD 23-MAR-1995.
XX
PF 15-SEP-1994; 94WO-US010469.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
XX
PA (VIAG-) VIAGENE INC.
XX
PI Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
XX
DR WPI; 1995-131362/17.
XX
PT New alpha virus vectors for gene therapy - of viral infection, cancer,
PT auto:immune disease, etc., and as vaccines.
XX
PS Example 7; Page 114; 260pp; English.
XX
CC The sequences given in AAQ86200-15 are primers which were used in the
CC production of alphavirus vectors expressing multiple heterologous genes.
CC These vectors are eukaryotic layered vector initiation systems (ELVIS)

Left column

```
CC   derived from Sindbis. ELVIS's comprise a 5' sequence capable of
CC   initiating transcription of an alphavirus, a nucleotide sequence encoding
CC   alphavirus non-structural proteins, a viral junction region which has
CC   been inactivated such that viral transcription of the subgenomic fragment
CC   is prevented, and an alphavirus RNA polymerase recognition sequence.
CC   Inactivation of the viral junction region prevents transcription of the
CC   subgenomic fragment making vectors such as this suitable for a wide
CC   variety of applications, eg. gene therapy for the treatment of cystic
CC   fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match             42.8%;  Score 24.4;  DB 2;  Length 52;
Best Local Similarity   59.4%;             Pred. No. 33;
Matches    19;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 UCCACCUCCGCGGUNNNNNNNUGGGCAUGCG 35
              :|||||:|||||:|         :|||||:||
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10
AAT31151
ID   AAT31151 standard; DNA; 52 BP.
XX
AC   AAT31151;
XX
DT   12-SEP-1996  (first entry)
XX
DE   HDV reverse primer HDV17-68.
XX
KW   Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
KW   polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;
KW   ribozyme; ss.
XX
OS   Synthetic.
XX
PN   WO9617072-A2.
XX
PD   06-JUN-1996.
XX
PF   30-NOV-1995;        95WO-US015490.
XX
PR   30-NOV-1994;        94US-00348472.
PR   18-JAN-1995;        95US-00376184.
PR   15-MAR-1995;        95US-00405827.
XX
PA   (CHIR ) CHIRON VIAGENE INC.
XX
PI   Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
PI   Belli BA;
XX
DR   WPI; 1996-277785/28.
XX
PT   New recombinant alpha-virus vectors - used to develop prods and methods
PT   for use in gene therapy and in the prodn. of vaccines.
XX
PS   Example 7; Page 120; 256pp; English.
XX
CC   Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)
CC   nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)
CC   for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV
CC   (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment
CC   contg. Sindbis 5'-end sequences. Overlapping
CC   synthesis is used in a second round of PCR using primers HDV49-XC and
CC   SIN276-SPE. The resulting construct contains the expression cassette
CC   elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction
CC   region/Sindbis structural protein genes/Sindbis 3'-end untranslated
CC   region, designated pd5'26s. This was inserted into pcDNA3. Packaging cell
CC   line cassettes were constructed that allow inducible expression of
CC   structural proteins via alphavirus vectors
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
```

Right column

```
Query Match             42.8%;  Score 24.4;  DB 2;  Length 52;
Best Local Similarity   59.4%;             Pred. No. 33;
Matches    19;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 UCCACCUCCGCGGUNNNNNNNUGGGCAUGCG 35
              :|||||:|||||:|         :|||||:||
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 11
AAT30817
ID   AAT30817 standard; DNA; 52 BP.
XX
AC   AAT30817;
XX
DT   12-SEP-1996  (first entry)
XX
DE   HDV ribozyme primer HDV17-68.
XX
KW   Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;
KW   polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;
KW   hepatitis delta virus; ss.
XX
OS   Synthetic.
XX
PN   WO9617072-A2.
XX
PD   06-JUN-1996.
XX
PF   30-NOV-1995;        95WO-US015490.
XX
PR   30-NOV-1994;        94US-00348472.
PR   18-JAN-1995;        95US-00376184.
PR   15-MAR-1995;        95US-00405827.
XX
PA   (CHIR ) CHIRON VIAGENE INC.
XX
PI   Dubensky TW,  Polo JM,  Ibanez CE,  Chang SMW,  Jolly DJ,  Driver DA;
PI   Belli BA;
XX
DR   WPI; 1996-277785/28.
XX
PT   New recombinant alpha-virus vectors - used to develop prods and methods
PT   for use in gene therapy and in the prodn. of vaccines.
XX
PS   Example 3; Page 85; 256pp; English.
XX
CC   primer SHDV1F (AAT30816) contains a buffer sequence allowing enzyme
CC   digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
CC   sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse
CC   primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic
CC   ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
CC   virus-based eukaryotic layered vector initiation system, ELVIS, and the
CC   transcription terminal signals to produce alphavirus expression vectors
CC   useful in methods of gene therapy and for vaccine prodn
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

RESULT 12
AAV42394
ID   AAV42394 standard; DNA; 52 BP.
XX
AC   AAV42394;
```

```
XX
DT   02-OCT-1998  (first entry)
XX
DE   Nested PCR primer HDV17-68 of the invention.
XX
KW   DNA alpha:virus; structural protein expression; inhibit; pathogen;
KW   immune response; stimulate; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5789245-A.
XX
PD   04-AUG-1998.
XX
PF   30-OCT-1996;       96US-00741881.
XX
PR   15-SEP-1993;       93US-00122791.
PR   18-FEB-1994;       94US-00198450.
PR   30-NOV-1994;       94US-00348472.
PR   20-JAN-1995;       95US-00376184.
PR   15-MAR-1995;       95US-00404796.
XX
PA   (CHIR )  CHIRON CORP.
XX
PI   Chang SMW, Ibanez CB, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX
DR   WPI; 1998-446089/38.
XX
PT   DNA alpha:virus structural protein expression cassettes - for producing
PT   recombinant alpha:virus particles.
XX
PS   Example 3; Col 69; 140pp; English.
XX
CC   PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC   invention. The specification describes a DNA alphavirus structural
CC   protein expression cassette which comprises an inducible promoter and an
CC   alphavirus structural protein gene, where the promoter directs the
CC   expression of the alphavirus structural protein gene upon induction of
CC   the promoter within a cell, and where prior to induction within the cell,
CC   the expression cassette does not express sufficient quantities of
CC   structural proteins to be cytotoxic to a BHK cell containing the
CC   expression cassette. The products may be used to inhibit pathogens and
CC   stimulate an immune response
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

     Query Match             42.8%;  Score 24.4;  DB 2;  Length 52;
     Best Local Similarity   59.4%;  Pred. No. 33;
     Matches  19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy          4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
              ::|||||:||:|||||:       :||||| ||
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13
AAV42426
ID   AAV42426 standard; DNA; 52 BP.
XX
AC   AAV42426;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Forward PCR primer HDV17-68.
XX
KW   DNA alpha:virus; structural protein expression; inhibit; pathogen;
KW   immune response; stimulate; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5789245-A.
XX
PD   04-AUG-1998.
```

```
XX
DT   30-OCT-1996;       96US-00741881.
XX
PF
PR   15-SEP-1993;       93US-00122791.
PR   18-FEB-1994;       94US-00198450.
PR   30-NOV-1994;       94US-00348472.
PR   20-JAN-1995;       95US-00376184.
PR   15-MAR-1995;       95US-00404796.
XX
PA   (CHIR )  CHIRON CORP.
XX
PI   Chang SMW, Ibanez CB, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX
DR   WPI; 1998-446089/38.
XX
PT   DNA alpha:virus structural protein expression cassettes - for producing
PT   recombinant alpha:virus particles.
XX
PS   Example 7; Col 103; 140pp; English.
XX
CC   PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC   invention. The specification describes a DNA alphavirus structural
CC   protein expression cassette which comprises an inducible promoter and an
CC   alphavirus structural protein gene, where the promoter directs the
CC   expression of the alphavirus structural protein gene upon induction of
CC   the promoter within a cell, and where prior to induction within the cell,
CC   the expression cassette does not express sufficient quantities of
CC   structural proteins to be cytotoxic to a BHK cell containing the
CC   expression cassette. The products may be used to inhibit pathogens and
CC   stimulate an immune response
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

     Query Match             42.8%;  Score 24.4;  DB 2;  Length 52;
     Best Local Similarity   59.4%;  Pred. No. 33;
     Matches  19;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy          4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
              ::|||||:||:|||||:       :||||| ||
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14
AAV60154
ID   AAV60154 standard; DNA; 52 BP.
XX
AC   AAV60154;
XX
DT   25-MAR-2003  (revised)
DT   04-DEC-1998  (first entry)
XX
DE   Nested PCR primer HDV17-68.
XX
KW   Eukaryotic layered vector initiation system; stimulate; immune response;
KW   Sindbis; PCR primer; ss.
XX
OS   Synthetic.
OS   Hepatitis D virus.
XX
PN   US5814482-A.
XX
PD   29-SEP-1998.
XX
PF   30-OCT-1996;       96US-00739158.
XX
PR   15-SEP-1993;       93US-00122791.
PR   18-FEB-1994;       94US-00198450.
PR   14-SEP-1994;       94WO-US010469.
PR   30-NOV-1994;       94US-00348472.
PR   18-JAN-1995;       95US-00376184.
PR   15-MAR-1995;       95US-00404796.
XX
PA   (POLO/)  POLO J M.
```

PA   (DUBE/) DUBENSKY T W.
PA   (JOLL/) JOLLY D J.
PA   (DRIV/) DRIVER D A.
XX
PI   Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX
DR   WPI; 1998-541753/46.
XX
PT   Eukaryotic layered vector initiation system - containing eukaryotic
PT   promoter and heterologous antigen coding sequence, useful for stimulating
PT   immune response.
XX
PS   Example 5; Col 108; 144pp; English.
XX
CC   PCR primers AAV60184-85 are used in the course of the invention. The
CC   specifiaction describes an eukaryotic layered vector initiation system,
CC   based on Sindbis. The eukaryotic layered vector initiation system
CC   comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC   susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
CC   The RNA comprises a vector construct which autonomously amplifies in the
CC   cell and expresses a heterologous nucleic acid sequence which encodes an
CC   antigen or modified form that stimulates an immune response within an
CC   animal. The system is useful for stimulating an immune response to an
CC   antigen by introducing the vector into target cells, preferably by
CC   infection in vivo, especially where the immune response is a cell
CC   mediated, HLA class I-restricted or an HLA class II-restricted immune
CC   response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match   42.8%; Score 24.4; DB 2; Length 52;
Best Local Similarity   59.4%; Pred. No. 33;
Matches   19; Conservative   6; Mismatches   7; Indels   0; Gaps   0;

Qy   4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
              :||||:||:|||||:   :||||| :||||
Db   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

Search completed: October 29, 2005, 08:21:09
Job time : 455 secs

PA   (DUBE/) DUBENSKY T W.
PA   (JOLL/) JOLLY D J.
PA   (DRIV/) DRIVER D A.
XX
PI   Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX
DR   WPI; 1998-541753/46.
XX
PT   Eukaryotic layered vector initiation system - containing eukaryotic
PT   promoter and heterologous antigen coding sequence, useful for stimulating
PT   immune response.
XX
PS   Example 3; Col 71-72; 144pp; English.
XX
CC   PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
CC   ribozyme sequence. The product is used in the course of the invention.
CC   The specifiaction describes an eukaryotic layered vector initiation
CC   system, based on Sindbis. The eukaryotic layered vector initiation system
CC   comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC   susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
CC   The RNA comprises a vector construct which autonomously amplifies in the
CC   cell and expresses a heterologous nucleic acid sequence which encodes an
CC   antigen or modified form that stimulates an immune response within an
CC   animal. The system is useful for stimulating an immune response to an
CC   antigen by introducing the vector into target cells, preferably by
CC   infection in vivo, especially where the immune response is a cell
CC   mediated, HLA class I-restricted or an HLA class II-restricted immune
CC   response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match   42.8%; Score 24.4; DB 2; Length 52;
Best Local Similarity   59.4%; Pred. No. 33;
Matches   19; Conservative   6; Mismatches   7; Indels   0; Gaps   0;

Qy   4 UCCACCUCCUCGCGGUNNNNNUGGGCAUGCG 35
              :||||:||:|||||:   :||||| :||||
Db   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15
AAV60185
ID   AAV60185 standard; DNA; 52 BP.
XX
AC   AAV60185;
XX
DT   25-MAR-2003 (revised)
DT   04-DEC-1998 (first entry)
XX
DE   Reverse PCR primer HDV17-68.
XX
KW   Eukaryotic layered vector initiation system; stimulate; immune response;
KW   Sindbis; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5814482-A.
XX
PD   29-SEP-1998.
XX
PF   30-OCT-1996;   96US-00739158.
XX
PR   15-SEP-1993;   93US-00122791.
PR   18-FEB-1994;   94US-00198450.
PR   14-SEP-1994;   94WO-US010469.
PR   30-NOV-1994;   94US-00348472.
PR   18-JAN-1995;   95US-00376184.
PR   15-MAR-1995;   95US-00404796.
XX
PA   (POLO/) POLO J M.
PA   (DUBE/) DUBENSKY T W.
PA   (JOLL/) JOLLY D J.
PA   (DRIV/) DRIVER D A.

```
                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:       October 29, 2005, 02:35:43 ; Search time 2993 Seconds
                                            (without alignments)
                                   724.913 Million cell updates/sec

Title:           US-09-699-667B-61
Perfect score:   57
Sequence:        1 gggtccaccucccgcggun.........uucgcauggcuaagggaccc 57

Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:      2048674

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_htc:*
               4: gb_est3:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_gss1:*
               9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
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Result No.		Score	Query Match %	Match Length	DB	ID	Description
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c	2	21.6	37.9	129	8	AZ937579	AZ937579 2M0195L18
c	3	21.2	37.2	141	4	BI007258	BI007258 MR1-RT007
c	4	21.2	37.2	147	1	AA094039	AA094039 c11641.se
c	5	21	36.8	148	2	BF368659	BF368659 QV1-GN006
c	6	20.6	36.1	114	1	AV848738	AV848738 AV848738
c	7	20.6	36.1	117	9	BX907242	BX907242 Leishmani
	8	20.6	36.1	117	1	LBAF063G06	LBAF063G06 Leishmani
c	9	20.6	36.1	118	1	AV855799	AV855799 AV855799
	10	20.6	36.1	135	8	CC043330	CC043330 3591_1_15
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c	13	20.2	35.4	125	4	AA856004	AA856004 vw8lf01.r
c	14	20.2	35.4	144	6	CD863939	CD863939 AZO1.108J
c	15	20.2	35.4	147	6	CD863940	CD863940 AZO1.108J
c	16	20	35.1	137	1	AA207969	AA207969 mv95f06.r
c	17	20	35.1	143	8	AZ407850	AZ407850 1M0178F14
c	18	19.8	34.7	61	7	CN482613	CN482613 hw22e05.y
c	19	19.8	34.7	105	8	BH215680	BH215680 1006028B0
c	20	19.8	34.7	108	2	AW401242	AW401242 LamdiGest
c	21	19.8	34.7	135	7	CO989014	CO989014 UMC-pd3en
c	22	19.6	34.4	145	8	BZ199525	BZ199525 CH230-444
c	23	19.6	34.4	112	4	BM286935	BM286935 527162 MA
c	24	19.6	34.4	119	8	BH173238	BH173238 0011B5 ma

c	25	19.6	34.4	123	4	BG693687	BG693687 344175 BA
c	26	19.6	34.4	136	8	BH035997	BH035997 RPCI-24-3
	27	19.6	34.4	140	8	CC019353	CC019353 3591_1_14
	28	19.6	34.4	146	4	BM746675	BM746675 K-EST0021
c	29	19.4	34.0	49	1	AI956143	AI956143 wt35e01.x
	30	19.4	34.0	117	4	BI021544	BI021544 CM3-MT034
	31	19.4	34.0	137	4	BI026587	BI026587 CM4-MT028
	32	19.4	34.0	147	2	BF768210	BF768210 PM1-CN010
	33	19.4	34.0	150	8	BH220875	BH220875 1006097G0
c	34	19.2	33.7	110	4	BM100180	BM100180 EBma01_SQ
c	35	19.2	33.7	116	4	BM029915	BM029915 488333_MA
c	36	19	33.3	111	7	CO788089	CO788089 NT003B_A0
c	37	19	33.3	120	1	AI153878	AI153878 ud50b05.r
	38	19	33.3	129	1	AA471148	AA471148 PMY2267 K
	39	19	33.3	136	8	BH616926	BH616926 SALK_0356
c	40	19	33.3	140	1	AV847196	AV847196 AV847196
c	41	19	33.3	148	2	BB482390	BB482390 BB482390
c	42	19	33.3	149	2	BB362950	BB362950 DG1_91_A0
c	43	18.8	33.0	73	4	BG035546	BG035546 60325605
c	44	18.8	33.0	85	6	CD036231	CD036231 mgnt011xI
c	45	18.8	33.0	90	8	AZ307919	AZ307919 1M001OD21

```
                          ALIGNMENTS

RESULT 1
AU077016/c
LOCUS       AU077016                 123 bp    mRNA    linear   EST 04-MAY-2000
DEFINITION  AU077016 Sugano cDNA library Homo sapiens cDNA clone Rp-A0037
            similar to 5'-end region of Human aminoacylase-1 (ACY1) mRNA, mRNA
            sequence.
ACCESSION   AU077016
VERSION     AU077016.1  GI:7439584
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 123)
AUTHORS     Suzuki,Y., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H.,
            Tsunoda,T., Watanabe,M., Komatsu,T., Ota,T., Isogai,T., Suyama,A.
            and Sugano,S.
TITLE       Statistical analysis of the 5' untranslated region of human mRNA
            using 'Oligo-Capped' cDNA libraries
JOURNAL     Genomics 64 (3), 286-297 (2000)
MEDLINE     20221373
PUBMED      10756096
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997)
            This clone was obtained from a 'full length-enriched' cDNA library
            constructed by 'Oligo-Capping' method. The coding region starts
            from the 50 bp upstream to the 3'-end.
FEATURES             Location/Qualifiers
     source          1..123
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="Rp-A0037"
                     /clone_lib="Sugano cDNA library"
ORIGIN

Query Match          42.1%;    Score 24; DB 1; Length 123;
Best Local Similarity 50.0%;    Pred. No. 5.8e+02;
Matches   23; Conservative   7; Mismatches  16; Indels   0; Gaps   0;
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```
Qy        4  UCCACCUCCUCGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGG  53
             :||:||:|||:||:|||        :||:||:||||| ||:||:|||
Db      112  TCCTCCTCCTCTTGGAATCCCGGGCCTCTGCCTTCTCTTGGTCAAGAG  63
```

RESULT 3
BI007258/c
LOCUS   BI007258   141 bp   mRNA   linear   EST 13-JUN-2001
DEFINITION   MR1-RT0079-220101-011-e07 RT0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI007258
VERSION   BI007258.1 GI:14411329
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 141)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR1&t2=MR1-RT0079-
              220101-011-e07&t3=2001-01-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 46
              High quality sequence stop: 122.
FEATURES   Location/Qualifiers
     source   1..141
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="RT0079"
                     /note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Query Match   37.2%; Score 21.2; DB 4; Length 141;
Best Local Similarity   43.8%; Pred. No. 5.6e+03;
Matches 21; Conservative   8; Mismatches 19; Indels   0; Gaps   0;

Qy   10 UCCCUGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
             ::|:| :||||||||:|||:||||:||::||| :| |||||||||
Db   98 TTCTCCATGTTGATGGTGGGGATGCTGTGTTCGGAGGAATAGGGTACCC 51
```

RESULT 4
AA094039/c
LOCUS         AA094039                147 bp    mRNA    linear   EST 25-OCT-1996
DEFINITION    cl1641.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
              cDNA 5', mRNA sequence.

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```
Qy        1  GGUCCACCUCCUCGCGGGUNNNNNUGGGCAUGCGGCUUCGCAUG  46
             |||:||  ||:||:||||| ||        :||:||:|||:||:||
Db      105  GGGTGCTCCTCCTCGGGACCCTTGCTGGTCATGGCCTGCGCGTGG  60
```

RESULT 2
AZ937579/c
LOCUS   AZ937579   129 bp   DNA   linear   GSS 26-APR-2001
DEFINITION   2M0195L18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
              clone UUGC2M0195L18 R, genomic survey sequence.
ACCESSION   AZ937579
VERSION   AZ937579.1 GI:13796530
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 129)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000   Std Error: 0.00
              Plate: 0195 row: L column: 18
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 129.
FEATURES   Location/Qualifiers
     source   1..129
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0195L18"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: pWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|, a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Query Match   37.9%; Score 21.6; DB 8; Length 129;
Best Local Similarity   46.0%; Pred. No. 4e+03;
Matches 23; Conservative   7; Mismatches 20; Indels   0; Gaps   0;
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ACCESSION   AA094039
VERSION     AA094039.1  GI:1639624
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 147)
AUTHORS     Liew,C.C.
TITLE       cDNAs from fetal heart (1996)
JOURNAL     Unpublished (1996)
COMMENT     Contact: Liew CC
            Brigham and Women's Hospital
            Harvard Medical School
            75 Francis St. Boston, MA 02115, USA
            Tel: 6177328915
            Fax: 6179750095
            Email: cliew@rics.bwh.harvard.edu
            PCR PRimers
            FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
            BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
            Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
FEATURES    Location/Qualifiers
     source 1..147
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /lab_host="E. coli XL1-Blue"
            /clone_lib="Human fetal heart, Lambda ZAP Express"
            /note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
            XhoI; mRNA was purified from human fetal hearts (8-10
            weeks). cDNA was synthesized using a XhoI-Oligo dT
            adaptor-primer. EcoRI adaptors were ligated, followed by
            digestion with XhoI, for directional cloning into
            predigested lambda ZAP Express."
ORIGIN

Query Match             37.2%;  Score 21.2;  DB 1;  Length 147;
Best Local Similarity   52.1%;  Pred. No. 5.6e+03;
Matches   25;  Conservative   4;  Mismatches  19;  Indels   0;  Gaps   0;

Qy    7 ACCUCGCCGGUNNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGA 54
          |||:||:|||||:  ||||| ||:|| |||
Db  115 ACCTTCCTCGGCGATTTTGGACTGGCACTCCGGCGGCTCATGCCAATAGGA 68

ORIGIN

RESULT 5
BF368659/c
LOCUS       BF368659     148 bp    mRNA     linear   EST 24-NOV-2000
DEFINITION  QV1-GN0063-290800-347-c02_1 GN0063 Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BF368659
VERSION     BF368659.1  GI:11330684
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 148)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QV1&t2=QV1-GN0063-
            290800-347-c02_1&t3=2000-08-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 148.
FEATURES    Location/Qualifiers
     source 1..148
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="GN0063"
            /note="Organ: placenta_normal; Vector: puc18; Site 1:
            SmaI; Site 2: SmaI; A mini-library was made by cloning
            products derived from ORESTES PCR (U.S. Letters Patent
            application No. 196,716 - Ludwig Institute for Cancer
            Research) profiles into the puc 18 vector. Reverse
            transcription of tissue mRNA and cDNA amplification were
            performed under low stringency conditions."
ORIGIN

Query Match             36.8%;  Score 21;  DB 2;  Length 148;
Best Local Similarity   43.1%;  Pred. No. 6.5e+03;
Matches   22;  Conservative   8;  Mismatches  21;  Indels   0;  Gaps   0;

Qy    3 GUCCACCUCCUCGCGGUNNNNNNNNUGGGCAUGCGGCCUUCGCAUGGCUAAGGG 53
          ||||||||||:  ||||||||
Db  137 GTCCACCTCCCAGGTGTGTTTCCTGAAGATGCTTGTACTTATGTCTAAGAG 87

ORIGIN

RESULT 6
AV848738/c
LOCUS       AV848738     114 bp    mRNA     linear   EST 08-NOV-2001
DEFINITION  AV848738 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone rciad14f13 3', mRNA sequence.
ACCESSION   AV848738
VERSION     AV848738.1  GI:16830368
KEYWORDS    EST.
SOURCE      Ciona intestinalis
ORGANISM    Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1 (bases 1 to 114)
AUTHORS     Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE       Expressed genes in Ciona intestinalis
JOURNAL     Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113.
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES    Location/Qualifiers
     source 1..114
            /organism="Ciona intestinalis"
            /mol_type="mRNA"
            /db_xref="taxon:7719"
            /clone="rciad14f13"
            /tissue_type="whole animal"
            /dev_stage="young adult"
            /clone_lib="Nori Satoh unpublished cDNA library, young
            adult"
ORIGIN

Query Match             36.1%;  Score 20.6;  DB 1;  Length 114;
Best Local Similarity   48.5%;  Pred. No. 8.9e+03;
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Matches   16; Conservative   7; Mismatches   10; Indels   0; Gaps   0;

Qy   13 UCGCGGUNNNNNUGGGCAGCGGCUUCGCAUG 45
                 :|||||: | :|:|||||||::||:|:|
Db   106 TCGCGGTGGCTGCTGCACCTGCGGCTTCGGATG 74

RESULT 7
BX907242
LOCUS   BX907242   117 bp   DNA   linear   GSS 07-JAN-2004
DEFINITION   Leishmania braziliensis GSS, clone LBAF063G06, genomic survey
              sequence.
ACCESSION   BX907242
VERSION   BX907242.1 GI:40735710
KEYWORDS   GSS; genomic survey sequence.
SOURCE   Leishmania braziliensis
  ORGANISM   Leishmania braziliensis
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Leishmania; Leishmania braziliensis species complex.
REFERENCE   1
  AUTHORS   Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.
  TITLE   GSS analysis of the Leishmania braziliensis genome
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 117)
  AUTHORS   Cruz,A.K.
  TITLE   Direct Submission
  JOURNAL   Submitted (07-JAN-2004) Cruz A.K., University of Sao Paulo,
              Department of Molecular and Cell Biology, FMRP, Avenida
              Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
COMMENT   Clone requests: akcruz@fmrp.usp.br.
FEATURES   Location/Qualifiers
     source   1..117
                     /organism="Leishmania braziliensis"
                     /mol_type="genomic DNA"
                     /strain="MHOM/BR/75/M2904"
                     /db_xref="taxon:5660"
                     /clone="LBAF063G06"
ORIGIN

Query Match   36.1%; Score 20.6; DB 9; Length 117;
Best Local Similarity 47.4%; Pred. No. 8.9e+03;
Matches   27; Conservative   5; Mismatches   25; Indels   0; Gaps   0;

Qy   1 GGGUCCACCUCCUCGCGCGGUNNNNNUGGGCAGCGGCUUCGCAUGGCUAAGGGACCC 57
                ||||| |:||| |||||||| | |::|||| || | : |:| |||||
Db   47 GCGCCCACTATCTCGGTCTCCACCTGCGGGCATCCCCCTCGGGATGTCGGAGGCACCC 103

RESULT 8
LBAF063G06
LOCUS   LBAF063G06   117 bp   DNA   linear   GSS 20-JUN-2003
DEFINITION   Leishmania braziliensis GSS, clone LBAF063G06, genomic survey
              sequence.
ACCESSION   BX543887
VERSION   BX543887.1 GI:32138222
KEYWORDS   GSS; genomic survey sequence.
SOURCE   Leishmania braziliensis
  ORGANISM   Leishmania braziliensis
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Leishmania; Leishmania braziliensis species complex.
REFERENCE   1
  AUTHORS   Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.
  TITLE   GSS analysis of the Leishmania braziliensis genome
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 117)
  AUTHORS   Cruz,A.K.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
              Department of Molecular and Cell Biology, FMRP, Avenida
              Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
COMMENT   Clone requests: akcruz@fmrp.usp.br.
FEATURES   Location/Qualifiers
     source   1..117

                     /organism="Leishmania braziliensis"
                     /mol_type="genomic DNA"
                     /strain="MHOM/BR/75/M2904"
                     /db_xref="taxon:5660"
                     /clone="LBAF063G06"
ORIGIN

Query Match   36.1%; Score 20.6; DB 9; Length 117;
Best Local Similarity 47.4%; Pred. No. 8.9e+03;
Matches   27; Conservative   5; Mismatches   25; Indels   0; Gaps   0;

Qy   1 GGGUCCACCUCCUCGCGCGGUNNNNNUGGGCAGCGGCUUCGCAUGGCUAAGGGACCC 57
                ||||| |:||| |||||||| | |::|||| || | : |:| |||||
Db   47 GCGCCCACTATCTCGGTCTCCACCTGCGGGCATCCCCCTCGGGATGTCGGAGGCACCC 103

RESULT 9
AV855799/c
LOCUS   AV855799   118 bp   mRNA   linear   EST 08-NOV-2001
DEFINITION   AV855799 Nori Satoh unpublished cDNA library, egg Ciona
              intestinalis cDNA clone rcieg19m19 3', mRNA sequence.
ACCESSION   AV855799
VERSION   AV855799.1 GI:16843323
KEYWORDS   EST.
SOURCE   Ciona intestinalis
  ORGANISM   Ciona intestinalis
              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cionidae; Ciona.
REFERENCE   1 (bases 1 to 118)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE   Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES   Location/Qualifiers
     source   1..118
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcieg19m19"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Nori Satoh unpublished cDNA library, egg"
ORIGIN

Query Match   36.1%; Score 20.6; DB 1; Length 118;
Best Local Similarity 48.5%; Pred. No. 8.9e+03;
Matches   16; Conservative   7; Mismatches   10; Indels   0; Gaps   0;

Qy   13 UCGCGGUNNNNNUGGGCAGCGGCUUCGCAUG 45
                 :|||||: | :|:|||||||::||:|:|
Db   110 TCGCGGTGGCTGCTGCACCTGCGGCTTCGGATG 78

RESULT 10
CC043330
LOCUS   CC043330   135 bp   DNA   linear   GSS 01-APR-2003
DEFINITION   3591_1_157_1_H10.y_1 3591 - RescueMu Grid P Zea mays genomic,
              genomic survey sequence.
ACCESSION   CC043330
VERSION   CC043330.1 GI:29458221
KEYWORDS   GSS.
SOURCE   Zea mays
  ORGANISM   Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 135)

AUTHORS   Walbot,V.
TITLE   Maize genomic sequences found using engineered RescueMu transposon
JOURNAL   Unpublished (2001)
COMMENT   Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855.California Ave. Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Possible ligation site so sequence was trimmed. Post-ligation
          sequence submitted separately.
          Plate: 3591_1_157_1 row: 29
          Class: transposon-tagged.
FEATURES   Location/Qualifiers
     source   1..135
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="3591 - RescueMu Grid P"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
                     extracted from leaf strips, double digested using BamHI
                     and BglII, and ligated to form circular plasmids. DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."
ORIGIN

Query Match   36.1%; Score 20.6; DB 8; Length 135;
Best Local Similarity   46.9%; Pred. No. 9e+03;
Matches .23; Conservative   6; Mismatches 20; Indels   0; Gaps   0;

Qy   9 CUCCUCGCCGUNNNNNNNUGGGCAUGCGGCAUUCGCAUGGCUAAGGGACCC 57
              |:|:|: ||: :|| |||||| ::|||||| | |||
Db   15 CTGCTGCTGGTCTGGTATGGACAGGCGGATTCGCAGTGGCCATGGCACAC 63

RESULT 11
BF875943
BF875943
LOCUS   BF875943   109 bp   mRNA   linear   EST 17-JAN-2001
DEFINITION CMO-ET0163-111100-687-g07 ET0163 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF875943
VERSION   BF875943.1 GI:12266073
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 109)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CMO&t2=CMO-ET0163-
111100-687-g07&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 109.
FEATURES   Location/Qualifiers
     source   1..109
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0163"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Query Match   35.4%; Score 20.2; DB 2; Length 109;
Best Local Similarity   53.8%; Pred. No. 1.2e+04;
Matches   21; Conservative   4; Mismatches 14; Indels   0; Gaps   0;

Qy   14 CGCGGUNNNNNNUGGGCAUGCGGCCUUCGCAUGCUAAGG 52
              ||||| :| | |||||| |||||||||::| |||
Db   9 CGCGGTTCTTACTGCGAAGGCGGCTTCTTACTGCGAAGG 47

RESULT 12
BE595364/c
LOCUS   BE595364   118 bp   mRNA   linear   EST 18-AUG-2000
DEFINITION PI1_53_C03.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
            mRNA sequence.
ACCESSION   BE595364
VERSION   BE595364.1 GI:9850437
KEYWORDS   EST.
SOURCE   Sorghum bicolor (sorghum)
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 118)
AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and
            Pratt,L.H.
TITLE   An EST database from Sorghum: pathogen-induced plants
JOURNAL   Unpublished (2000)
COMMENT   Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            An EST database from Sorghum: pathogen-induced plants
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: JEN REV
            High quality sequence stop: 100
            POLYA=No.
FEATURES   Location/Qualifiers
     source   1..118
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /db_xref="taxon:4558"
                     /clone_lib="Pathogen induced 1 (PI1)"

/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site 1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX-623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."

ORIGIN

Query Match   35.4%;   Score 20.2; DB 2; Length 118;
Best Local Similarity   49.1%; Pred. No. 1.2e+04;
Matches   27;   Conservative   4; Mismatches   24;   Indels   0;   Gaps   0;

Qy   1 GGGUCCACCUCCGCGGUNNNNNNUGGGGACCAUGGCUUCGCAUGGCUAAGGGAC 55
          ||||||| :|:|||| ||:|||||:|| ||||||
Db   69 GGAGCCATCAGTCGCGCATGAACTGAAGCAGAAGGTTTGCCATGGCAATGGGAC 15

RESULT 13
AA856004/c
LOCUS   AA856004   125 bp   mRNA   linear   EST 06-MAR-1998
DEFINITION vw81f01.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
            IMAGE:1261369 5', mRNA sequence.
ACCESSION   AA856004
VERSION   AA856004.1 GI:2943542
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 125)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE   The WashU-HHMI Mouse EST Project
JOURNAL   Unpublished (1996)
COMMENT   Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:663921
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 112.
FEATURES   Location/Qualifiers
     source   1..125
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1261369"
                     /sex="females"
                     /tissue_type="whole skin"
                     /dev_stage="11 weeks old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse skin (#937313)"
                     /note="Organ: skin; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match   35.4%;   Score 20.2; DB 1; Length 125;
Best Local Similarity   50.9%; Pred. No. 1.2e+04;
Matches   28;   Conservative   3; Mismatches   24;   Indels   0;   Gaps   0;

Qy   2 GGUCCACCUCCGCGGUNNNNNNUGGGGACCAUGGCGGCUUCGCAUGGCUAAGGGACC 56
          ||||||| :|:||| |||:|| ||||||:|| ||||||
Db   119 GGGCCACGTCTCTGGGGCGCGCAGGGCGGAGGCGCGTACTTGCGGCCGCAGGGAGC 65

RESULT 14
CD863939/c
LOCUS   CD863939   144 bp   mRNA   linear   EST 11-JUL-2003
DEFINITION AZO1.108U17F010131 AZO1 Triticum aestivum cDNA clone AZO1108J17,
            mRNA sequence.
ACCESSION   CD863939
VERSION   CD863939.1 GI:32547755
KEYWORDS   EST.
SOURCE   Triticum aestivum (bread wheat)
ORGANISM   Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 144)
AUTHORS   Genoplante.
TITLE   Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES   Location/Qualifiers
     source   1..144
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="recital"
                     /db_xref="taxon:4565"
                     /clone="AZO1108J17"
                     /tissue_type="leaf"
                     /clone_lib="AZO1"

ORIGIN

Query Match   35.4%;   Score 20.2; DB 6; Length 144;
Best Local Similarity   45.5%; Pred. No. 1.2e+04;
Matches   25;   Conservative   6; Mismatches   24;   Indels   0;   Gaps   0;

Qy   3 GUCCACCUCCGCGGUNNNNNNUGGGGACCAUGGCGGCUUCGCAUGGCUAAGGGACCC 57
          |:|:|:|| | |:|| |||||| ||| |||||
Db   124 GTGCTCCTCCAGGCCGTCGGCGTCCCGCCGTGCCCGTGCCGCTTGGCGAACCGGCCC 70

RESULT 15
CD863940
LOCUS   CD863940   147 bp   mRNA   linear   EST 11-JUL-2003
DEFINITION AZO1.108U17R010507 AZO1 Triticum aestivum cDNA clone AZO1108J17,
            mRNA sequence.
ACCESSION   CD863940
VERSION   CD863940.1 GI:32547756
KEYWORDS   EST.
SOURCE   Triticum aestivum (bread wheat)
ORGANISM   Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```
REFERENCE    Pooideae; Triticeae; Triticum.
             1 (bases 1 to 147)
AUTHORS      Genoplante.
TITLE        Genoplante, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplante
             Genoplante
             93, rue Henri Rochefort 91025 EVRY CEDEX France
             Tel: 33 1 69 47 54 00
             Fax: 33 1 69 47 54 10
             This sequence has been generated in the framework of the french
             plant genomics programme 'Genoplante' (http://www.genoplante.com
             and http://genoplante-info.infobiogen.fr).
FEATURES     Location/Qualifiers
     source  1..147
             /organism="Triticum aestivum"
             /mol_type="mRNA"
             /cultivar="recital"
             /db_xref="taxon:4565"
             /clone="AZ0110BJ17"
             /tissue_type="leaf"
             /clone_lib="AZO1"

ORIGIN

Query Match              35.4%;    Score 20.2;  DB 6;  Length 147;
Best Local Similarity    45.5%;    Pred. No. 1.2e+04;
Matches  25;  Conservative   6;  Mismatches   24;  Indels   0;  Gaps   0;

Qy   3 GUCCACCUCCUCGCGGUNNNNNNUGGGCAUGCGGCUUCGGCAUGGCUAAGGGACCC 57
       |:| ||:||| ||  ||   | :|| | |:||  : ||| :||| ||||| |||| |||
Db  25 GTGCTCCTCCAGGCCGTCGGCGTCCGCCGTGCCCGTGCCCGTGGCGAACCGGCCC 79

Search completed: October 29, 2005, 09:39:59
Job time : 3002 secs
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                 GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:     October 29, 2005, 01:30:12 ; Search time 1709 Seconds
                                 (without alignments)
                          1616.119 Million cell updates/sec

Title:      US-09-699-667E-61
Perfect score:  57
Sequence:   1 ggguccaccuccucgcggun.........uucgcauggcuaagggaccc 57

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:   4708233 seqs, 2422760795 residues

Total number of hits satisfying chosen parameters:    2505164

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
     1: gb_ba:*
     2: gb_htg:*
     3: gb_in:*
     4: gb_om:*
     5: gb_ov:*
     6: gb_pat:*
     7: gb_ph:*
     8: gb_pl:*
     9: gb_pr:*
    10: gb_ro:*
    11: gb_sts:*
    12: gb_sy:*
    13: gb_un:*
    14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES

                  %
Result           Query
No.    Score   Match  Length DB   ID          Description
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  1     51     89.5     57    6   AX012282    AX012282 Sequence
  2     51     89.5     57    6   AX012283    AX012283 Sequence
  3     51     89.5     57    6   AX012285    AX012285 Sequence
  4     51     89.5     57    6   AX012286    AX012286 Sequence
  5     51     89.5     57    6   AX012287    AX012287 Sequence
  6     51     89.5     57    6   AX012288    AX012288 Sequence
  7     51     89.5     57    6   AX012289    AX012289 Sequence
  8     51     89.5     57    6   AX012290    AX012290 Sequence
  9    41.4    72.6     57    6   AX012291    AX012291 Sequence
 10     31     54.4     37    6   I41390      I41390 Sequence 18
 11    25.8    45.3     61    6   AR021007    AR021007 Sequence
 12    24.4    42.8     52    6   AR021047    AR021047 Sequence
 13    24.4    42.8     52    6   AR043422    AR043422 Sequence
 14    24.4    42.8     52    6   AR043462    AR043462 Sequence
 15    24.4    42.8     52    6   AR062337    AR062337 Sequence
 16    24.4    42.8     52    6   AR062377    AR062377 Sequence
 17    24.4    42.8     52    6   AR183796    AR183796 Sequence
 18    24.4    42.8     52    6   AR183836    AR183836 Sequence
 19    24.4    42.8     52    6   AR368179    AR368179 Sequence
 20    24.4    42.8     52    6   AR368219    AR368219 Sequence
 21    24.4    42.8     52    6   AR368219    AR368219 Sequence
 22    24.4    42.8     57    6   CQ759677    CQ759677 Sequence
 23    24.4    42.8     80    6   I41388      I41388 Sequence 16
 24    24.4    42.8     83    6   AR123021    AR123021 Sequence
 25    24.4    42.8     84    6   I41385      I41385 Sequence 13
 26    24.4    42.8     84    6   I41386      I41386 Sequence 14
 27    24.4    42.8     86    6   I41378      I41378 Sequence 6
 28    24.4    42.8     90    6   BD226817    BD226817 Alphaviru
 29    24.4    42.8     90    6   AR243300    AR243300 Sequence
 30    24.4    42.8     90    6   AR342596    AR342596 Sequence
 31  c 24.4    42.8     90    6   AR342597    AR342597 Sequence
 32    24.4    42.8     90    6   AX174838    AX174838 Sequence
 33  c 24.4    42.8     90    6   AX174839    AX174839 Sequence
 34    24.4    42.8    101    6   AR363756    AR363756 Sequence
 35  c 24.4    42.8    105    6   A41844      A41844 Sequence 25
 36  c 24.4    42.8    105    6   A41849      A41849 Sequence 30
 37    23.6    41.4     85    6   I41384      I41384 Sequence 12
 38     23     40.4     56    6   AR221187    AR221187 Sequence
 39     23     40.4     56    6   AR230614    AR230614 Sequence
 40     23     40.4     56    6   AR234088    AR234088 Sequence
 41     23     40.4     56    6   AR237698    AR237698 Sequence
 42     23     40.4     56    6   AR353208    AR353208 Sequence
 43     23     40.4     56    6   BD078782    BD078782 Recombina
 44     23     40.4     56    6   BD085609    BD085609 Recombina
 45     23     40.4     71    6   I41387      I41387 Sequence 15


                        ALIGNMENTS

RESULT 1
AX012282
LOCUS       AX012282         57 bp    RNA      linear   PAT 06-SEP-2000
DEFINITION  Sequence 44 from Patent WO9955856.
ACCESSION   AX012282
VERSION     AX012282.1  GI:9998343
KEYWORDS
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 44 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES             Location/Qualifiers
     source          1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

Query Match             89.5%;  Score 51;  DB 6;  Length 57;
Best Local Similarity   71.9%;  Pred. No. 4.5e-06;
Matches   41;  Conservative  10;  Mismatches  6;  Indels  0;  Gaps  0;

Qy          1 GGGUCCACCUCCUCGCGGUNNNNNNUGGGCAUGCGGCGUUCCGCAUGGCUAAGGGACCC 57
              ||||:||||||:||::|||||          ::||||:|||||::|||||:||:|||||||||
Db          1 GGGUCCACCUCCUCGCGGUCCGACCUGGGCAUGCGGCGUUCGCAUGGCUAAGGGACCC 57

RESULT 2
AX012283
LOCUS       AX012283         57 bp    RNA      linear   PAT 06-SEP-2000
DEFINITION  Sequence 45 from Patent WO9955856.
ACCESSION   AX012283
VERSION     AX012283.1  GI:9998344
KEYWORDS
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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```
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 995856-A 45 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES             Location/Qualifiers
     source          1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

  Query Match             89.5%;  Score 51;  DB 6;  Length 57;
  Best Local Similarity   71.9%;  Pred. No. 4.5e-06;
  Matches    41;  Conservative    10;  Mismatches   6;  Indels    0;  Gaps    0;

Qy          1 GGGUCCACCUCCUCGCGGUNNNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
              ||||||||||||||||||:||||||:        :|||||||||||:||||||||||||
Db          1 GGGUCCACCUCCUCGCGGUCCCAGCUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57


RESULT 3
AX012285
LOCUS       AX012285                  57 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 47 from Patent WO9955856.
ACCESSION   AX012285
VERSION     AX012285.1  GI:9998346
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 47 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES             Location/Qualifiers
     source          1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

  Query Match             89.5%;  Score 51;  DB 6;  Length 57;
  Best Local Similarity   71.9%;  Pred. No. 4.5e-06;
  Matches    41;  Conservative    10;  Mismatches   6;  Indels    0;  Gaps    0;

Qy          1 GGGUCCACCUCCUCGCGGUNNNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
              ||||||||||||||||||:||||||:        :|||||||||||:||||||||||||
Db          1 GGGUCCACCUCCUCGCGGUCCCCCUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57


RESULT 4
AX012286
LOCUS       AX012286                  57 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 48 from Patent WO9955856.
ACCESSION   AX012286
VERSION     AX012286.1  GI:9998347
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 48 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
```

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FEATURES             Location/Qualifiers
     source          1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

  Query Match             89.5%;  Score 51;  DB 6;  Length 57;
  Best Local Similarity   71.9%;  Pred. No. 4.5e-06;
  Matches    41;  Conservative    10;  Mismatches   6;  Indels    0;  Gaps    0;

Qy          1 GGGUCCACCUCCUCGCGGUNNNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
              ||||||||||||||||||:|||||||:       :|||||||||:||||||||||||
Db          1 GGGUCCACCUCCUGCGGUCCGGGUCCGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57


RESULT 5
AX012287
LOCUS       AX012287                  57 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 49 from Patent WO9955856.
ACCESSION   AX012287
VERSION     AX012287.1  GI:9998348
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 995856-A 49 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES             Location/Qualifiers
     source          1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

  Query Match             89.5%;  Score 51;  DB 6;  Length 57;
  Best Local Similarity   71.9%;  Pred. No. 4.5e-06;
  Matches    41;  Conservative    10;  Mismatches   6;  Indels    0;  Gaps    0;

Qy          1 GGGUCCACCUCCUCGCGGUNNNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
              ||||||||||||||||||:|||||||:       :|||||||||:||||||||||||
Db          1 GGGUCCACCUCCUGCGGUCCGGGUCCGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57


RESULT 6
AX012288
LOCUS       AX012288                  57 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 50 from Patent WO9955856.
ACCESSION   AX012288
VERSION     AX012288.1  GI:9998349
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 995856-A 50 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN
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Query Match   89.5%; Score 51; DB 6; Length 57;
Best Local Similarity   71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches   6; Indels   0; Gaps   0;

Qy 1 GGGUCCACCUCCGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
        ||:|||||:||:||||::   :||||||||||||||||||||||||||||
Db 1 GGGUCCACCUCCUCGCGGUCCGCGGUCCGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57

RESULT 7
AX012289
LOCUS   AX012289   57 bp   RNA   linear   PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION   AX012289
VERSION   AX012289.1 GI:9998350
KEYWORDS
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE   Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 51 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES   Location/Qualifiers
     source   1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

Query Match   89.5%; Score 51; DB 6; Length 57;
Best Local Similarity   71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches   6; Indels   0; Gaps   0;

Qy 1 GGGUCCACCUCCGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
        ||:|||||:||:||||::   :||||||||||||||||||||||||||||
Db 1 GGGUCCACCUCCUCGCGGUCCGAGCUGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57

RESULT 8
AX012290
LOCUS   AX012290   57 bp   RNA   linear   PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION   AX012290
VERSION   AX012290.1 GI:9998351
KEYWORDS
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE   Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 52 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES   Location/Qualifiers
     source   1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

Query Match   89.5%; Score 51; DB 6; Length 57;
Best Local Similarity   71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches   6; Indels   0; Gaps   0;

Qy 1 GGGUCCACCUCCGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
        ||:|||||:||:|||||:

Right column

Db 1 GGGUCCACCUCCGCGGUCCGAUCUGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57

RESULT 9
AX012284
LOCUS   AX012284   57 bp   RNA   linear   PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION   AX012284
VERSION   AX012284.1 GI:9998345
KEYWORDS
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE   Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 46 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES   Location/Qualifiers
     source   1..57
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

Query Match   72.6%; Score 41.4; DB 6; Length 57;
Best Local Similarity   64.9%; Pred. No. 0.0057;
Matches 37; Conservative   8; Mismatches   12; Indels   0; Gaps   0;

Qy 1 GGGUCCACCUCCGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
        |||:|||||:||:||||| :||||||||||||||||||||||||||
Db 1 GGGUCCACCUCCGCGGUCCGACCUGGGCAUGCGGCAUGCCUAAGGACCC 57

RESULT 10
AX012291
LOCUS   AX012291   37 bp   RNA   linear   PAT 06-SEP-2000
DEFINITION Sequence 53 from Patent WO9955856.
ACCESSION   AX012291
VERSION   AX012291.1 GI:9998352
KEYWORDS
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE   Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 53 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

Query Match   54.4%; Score 31; DB 6; Length 37;
Best Local Similarity   67.6%; Pred. No. 14;
Matches 25; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy 1 GGGUCCACCUCCGCGGUNNNNNUGGGCAUGCGGC 37
        |||:|||||:||:||||| :|||||||
Db 1 GGGUCCACCUCCGCGGUCCGACCUGGGCAUGCGGC 37

RESULT 11
I41390
LOCUS   I41390   61 bp   DNA   linear   PAT 13-MAY-1997
DEFINITION Sequence 18 from patent US 5625047.

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ACCESSION   I41390
VERSION     I41390.1  GI:2081980
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 61)
AUTHORS     Been,M.D., Rosenstein,S.P. and Perrotta,A.T.
TITLE       Enzymatic RNA molecules
JOURNAL     Patent: US 5625047-A 18 29-APR-1997;
FEATURES             Location/Qualifiers
     source          1..61
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             45.3%;  Score 25.8;  DB 6;  Length 61;
  Best Local Similarity 58.5%;  Pred. No. 6.3e+02;
  Matches   31;  Conservative   10;  Mismatches    8;  Indels    4;  Gaps    1;

Qy          4 UCCACCUCCGCGGUNNNNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACC 56
              :||||||:||:||||||:   :|||||:   |:||: |||||:||||||
Db          8 TCCACCTCCTCGCGGTCCGACCTGGGCAT---CTTCGGATGGCTAAGGGAGC 56


RESULT 12
LOCUS       AR021007                  52 bp   DNA        linear   PAT 05-DEC-1998
DEFINITION  Sequence 40 from patent US 5789245.
ACCESSION   AR021007
VERSION     AR021007.1  GI:3975622
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
AUTHORS     Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
            and Driver,D.A.
TITLE       Alphavirus structural protein expression cassettes
JOURNAL     Patent: US 5789245-A 40 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1..52
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             42.8%;  Score 24.4;  DB 6;  Length 52;
  Best Local Similarity 59.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
              :||||||:||:||||||:   :||||: |
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 13
LOCUS       AR021047                  52 bp   DNA        linear   PAT 05-DEC-1998
DEFINITION  Sequence 80 from patent US 5789245.
ACCESSION   AR021047
VERSION     AR021047.1  GI:3975662
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
AUTHORS     Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
            and Driver,D.A.
TITLE       Alphavirus structural protein expression cassettes
JOURNAL     Patent: US 5789245-A 80 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1..52
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             42.8%;  Score 24.4;  DB 6;  Length 52;
  Best Local Similarity 59.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
              :||||||:||:||||||:   :||||: |
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 14
LOCUS       AR043422                  52 bp   DNA        linear   PAT 29-SEP-1999
DEFINITION  Sequence 40 from patent US 5814482.
ACCESSION   AR043422
VERSION     AR043422.1  GI:5964430
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
AUTHORS     Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE       Eukaryotic layered vector initiation systems
JOURNAL     Patent: US 5814482-A 40 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..52
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             42.8%;  Score 24.4;  DB 6;  Length 52;
  Best Local Similarity 59.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
              :||||||:||:||||||:   :||||: |
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


RESULT 15
LOCUS       AR043462                  52 bp   DNA        linear   PAT 29-SEP-1999
DEFINITION  Sequence 80 from patent US 5814482.
ACCESSION   AR043462
VERSION     AR043462.1  GI:5964470
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
AUTHORS     Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE       Eukaryotic layered vector initiation systems
JOURNAL     Patent: US 5814482-A 80 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..52
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             42.8%;  Score 24.4;  DB 6;  Length 52;
  Best Local Similarity 59.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 UCCACCUCCGCGGUNNNNNUGGGCAUGCG 35
              :||||||:||:||||||:   :||||: |
Db          1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32


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OM nucleic - nucleic search, using sw model

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          Copyright (c) 1993 - 2005 Compugen Ltd.

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   96:  /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
   97:  /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
   98:  /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
   99:  /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
  100:  /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
  101:  /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
  102:  /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
  103:  /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
  104:  /cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
  105:  /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
  106:  /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
  107:  /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
  108:  /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
  109:  /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
  110:  /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
  111:  /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
  112:  /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
  113:  /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
  114:  /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
  115:  /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
  116:  /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
  116:  /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*
```

117:    /cgn2_6/ptcodata/1/pna/US6047_COMB.seq:*
118:    /cgn2_6/ptcodata/1/pna/US6048_COMB.seq:*
119:    /cgn2_6/ptcodata/1/pna/US6049_COMB.seq:*
120:    /cgn2_6/ptcodata/1/pna/US6050_COMB.seq:*
121:    /cgn2_6/ptcodata/1/pna/US6051_COMB.seq:*
122:    /cgn2_6/ptcodata/1/pna/US6052_COMB.seq:*
123:    /cgn2_6/ptcodata/1/pna/US6053_COMB.seq:*
124:    /cgn2_6/ptcodata/1/pna/US6054_COMB.seq:*
125:    /cgn2_6/ptcodata/1/pna/US6055_COMB.seq:*
126:    /cgn2_6/ptcodata/1/pna/US6056_COMB.seq:*
127:    /cgn2_6/ptcodata/1/pna/US6057_COMB.seq:*
128:    /cgn2_6/ptcodata/1/pna/US6058_COMB.seq:*
129:    /cgn2_6/ptcodata/1/pna/US6059_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   Query
No.   Score   Match Length DB ID   Description

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2005, 08:21:20 ; Search time 1990 Seconds
                                     (without alignments)
                                     411.830 Million cell updates/sec

Title: US-09-699-667E-61
Perfect score: 57
Sequence: 1 ggguccaccuccgcggun........uucgcauggcuaagggaccc 57

Scoring table: IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27723106 seqs, 718968421 residues

Total number of hits satisfying chosen parameters: 40003802

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_NA_New:*
                 1: /cgn2_6/ptodata71/pna/PCT_NEW_COMB.seq:*
                 2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2:*
                 3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
                 4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
                 5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
                 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
                 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1:*
                 8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
                 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
                 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq10:*
                 11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq11:*
                 12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
                 13: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
                 14: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4:*
                 15: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq5:*
                 16: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq6:*
                 17: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq7:*
                 18: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq8:*
                 19: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq9:*
                 20: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
                 21: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
                 22: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3:*
                 23: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq4:*
                 24: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq5:*
                 25: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq6:*
                 26: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq7:*
                 27: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq8:*
                 28: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   Query
No.   Score   Match Length DB   ID   Description

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